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(FILE 'HOME' ENTERED AT 12:08:36 ON 05 APR 2004)

FILE 'DISSABS, IMOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 12:08:46 ON
05 APR 2004

E 'SAINT-REMY' 'JEAN-MARIE'?/AU

E SAINT-REMY JEAN-MARIE?/AU

E JACQUEMIN MARC?/AU

L1 50 S E1 OR E2
L2 652376 S (SYSTEMIC INFLAMMATORY RESPONSE SYNDROME) OR SIRS OR SEPSIS O
L3 100225 S FACTOR (A) VIII
L4 3552 S (ANTI OR ANTIBOD?) (A) L3
L5 29 S L4 (S) L2
L6 20 DUP REM L5 (9 DUPLICATES REMOVED)

=>

WEST Search History

DATE: Monday, April 05, 2004

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L13	L11 same l4	5
<input type="checkbox"/>	L12	L11 same l3	2
<input type="checkbox"/>	L11	hemophilia adj a	839
<input type="checkbox"/>	L10	L6 same l4	1
<input type="checkbox"/>	L9	L5 same l4	159
<input type="checkbox"/>	L8	L5 same l3	8
<input type="checkbox"/>	L7	L6 same l3	1
<input type="checkbox"/>	L6	(anti or antibod\$) adj L5	275
<input type="checkbox"/>	L5	factor adj (VIII or V)	8473
<input type="checkbox"/>	L4	sepsis or septic or thrombus	36439
<input type="checkbox"/>	L3	(systemic inflammatory response syndrome) or SIRS	40826
<input type="checkbox"/>	L2	Jacquemin-marc-\$.in.	4
<input type="checkbox"/>	L1	'Saint-remy'-'Jean-Marie'-.in.	4

END OF SEARCH HISTORY

L6 ANSWER 8 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 1999:465724 CAPLUS

DOCUMENT NUMBER: 131:115050

TITLE: Antibodies against factor VIII in patients with solid tumors. Successful treatment of cancer may suppress inhibitor formation

AUTHOR(S): Sallah, Sabah; Singh, Paramjeet; Hanrahan, L. Robert

CORPORATE SOURCE: Department Medicine, Division Hematology/Oncology, Univ. Tennessee, Memphis, TN, 38163, USA

SOURCE: Haemostasis (1998), 28(5), 244-249

CODEN: HMTSB7; ISSN: 0301-0147

PUBLISHER: S. Karger AG

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In 1995-1998, the authors treated 5 patients with anti-factor VIII antibodies and spontaneous bleeding. All patients had underlying malignant conditions. Initial control of the bleeding episodes and reduction in inhibitor titer was achieved in all patients. Disappearance of factor VIII inhibitor occurred in 3 patients after either resection of the tumor or chemotherapy. Immunosuppression therapy failed to eradicate the antibody in 2 patients with metastatic disease. Antibodies against factor VIII appearing in certain patients may be directly associated with the underlying malignancy, rather than a coincidental finding. Attempts to reduce the titer or eradicate the inhibitor may fail if recognition of the underlying condition is not sought, or an appropriate treatment of cancer is not offered. Antibodies against factor VIII developing in previously healthy individuals constitute the most common spontaneous inhibitors of any clotting factor. Accurate ests. of the incidence of **anti-factor VIII** inhibitors are not available, since some of these antibodies may not be associated with bleeding, or the condition may be misinterpreted as **disseminated intravascular coagulation**, especially when it is associated with known underlying malignancy. About 50% of anti-factor VIII antibodies developing in the nonhemophilic population occur in otherwise healthy individuals over the age of 50 yr. Other conditions associated with the development of these inhibitors, in decreasing frequency, include autoimmune diseases, peripartum period, lymphoproliferative disorders, solid tumors and reaction to certain medications [1]. Patients with antibodies against factor VIII usually present with spontaneous bleedings involving soft tissues, retropharyngeal or retroperitoneal spaces, intracerebral or other types of serious hemorrhagic episodes. The most common laboratory abnormality is prolongation of PTT and decreased to absent factor VIII activity. Among the most commonly used products to manage patients with bleeding episodes and autoantibodies against factor VIII are high-dose human factor VIII, and inhibitor by-passing agents. Decreasing the inhibitor titer may also be achieved via plasma exchange and immuno-suppression. The formation of factor VIII antibodies in patients with solid tumors in terms of its course, response to treatment, and prognosis has not been addressed. We describe in this article the occurrence and the course of anti-factor VIII antibodies in 5 patients with solid malignancies.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN T

ACCESSION NUMBER: 2001:70012 CAPLUS
DOCUMENT NUMBER: 135:32107
TITLE: Transient factor VIII inhibitor in a hemophilia
patient after staphylococcal septic shock syndrome
AUTHOR(S): Yamamoto, Kazuhiko; Niiya, Kenji; Shigematu, Terunobu;
Kiguchi, Toru; Takenaka, Katsuto; Shinagawa, Katsushi;
Ishimaru, Fumihiko; Ikeda, Kazuma; Shima, Midori;
Harada, Mine
CORPORATE SOURCE: Second Department of Medicine, Okayama University
Medical School, Okayama, 700-8558, Japan
SOURCE: International Journal of Hematology (2000), 72(4),
517-519
CODEN: IJHEEY; ISSN: 0925-5710
PUBLISHER: Carden Jennings Publishing
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We report a transient type I factor VIII inhibitor that arose in a 30-yr-old hemophilia patient just after staphylococcal septicemia. This situation usually occurs early in the course of substitution therapy with factor VIII concentrate in hemophilia patients. Although disseminated intravascular coagulation and acute respiratory distress syndrome developed after septic shock, the patient recovered following i.v. administration of antibiotics (meropenem and gentamycin), an antithrombin preparation, high-dose methylprednisolone, and recombinant factor VIII concentrate (rFVIII). During this therapy, however, activated partial thromboplastin time gradually lengthened. On the seventh day of hospitalization, intracranial hemorrhage occurred with right hemiplegia, even though the substitution therapy had continued at the same dosage (30 U/kg per day) of rFVIII. At that point, 4 Bethesda units of the type I inhibitor against factor VIII were detected in the plasma. Increased amts. (46 U/kg per day) of rFVIII and prednisolone were administered, and hypothermic therapy was initiated. Following these treatments, the patient's general condition gradually improved, and within 25 days the inhibitor titer dropped to undetectable levels and did not recur during treatment. These clin. findings suggest that the staphylococcal septic shock may have acted as a trigger in the development of transient factor VIII inhibitor in this patient.


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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-862-124-5
Query Match 88.0%; Score 649.5; DB 3; Length 150;
Best Local Similarity 87.7%; Pred. No. 3.2e-54;
Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 5 MEFAQLLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSVSSYLAWYQOK 64
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSS--AL 117
DB 65 PGQAPRLLIYGASTRATGMDRSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSPQTPO 124
QY 118 LTGGGKVEIKRTVAAPSVFIIPPS 143
DB 125 ITFGGKVEIKRTVAAPSVFIIPPS 150

RESULT 6
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-17
Query Match 87.4%; Score 645; DB 4; Length 234;
Best Local Similarity 90.9%; Pred. No. 1.4e-53;
Matches 130; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

QY 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSV--SSYLAWYQOK 59
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSSALLTF 120
DB 60 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSP-FTF 118
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 119 GPGTKVDIKRTVAAPSVFIIPPS 141

RESULT 8
US-08-405-034-4
; Sequence 4, Application US/08405034
; Patent No. 5744585
; Patent No. 5744585 5712371
; GENERAL INFORMATION:
; APPLICANT: Medenica, Rajko D.
; APPLICANT: Mukerjee, Sonjoy
; TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
; TITLE OF INVENTION: Carcinoma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
QY 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSV--SSYLAWYQOK 59
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSSALLTF 120
DB 60 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSP-FTF 118
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 119 GPGTKVDIKRTVAAPSVFIIPPS 141

RESULT 8
US-08-405-034-4
; Sequence 4, Application US/08405034
; Patent No. 5744585
; Patent No. 5744585 5712371
; GENERAL INFORMATION:
; APPLICANT: Medenica, Rajko D.
; APPLICANT: Mukerjee, Sonjoy
; TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
; TITLE OF INVENTION: Carcinoma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
QY 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLWLPDITGTEIVLTQPGTSLSPGERATLSCRASQSV--SSYLAWYQOK 59
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSSALLTF 120
DB 60 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSP-FTF 118
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 119 GPGTKVDIKRTVAAPSVFIIPPS 141
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/
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/405,034
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sara, Charles S.
/ REGISTRATION NUMBER: 30,492
/ REFERENCE/DOCKET NUMBER: 34656.009
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-831-2100
/ TELEFAX: 608-831-2106
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 134 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-405-034-4

Query Match      81.8%; Score 604; DB 1; Length 134;
Best Local Similarity 88.1%; Pred. No. 5.5e-50;
Matches 118; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 METPAQLLLFLLLLWLPDTTGGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLFLLLLWLPDTTGGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFF 120
DB 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFF 120

QY 121 GGGTKVEIKRTVAA 134
DB 121 GGGTKVEIKRTVAA 134

RESULT 9
US-08-480-774A-4
/ Sequence 4, Application US/08480774A
/ Patent No. 5852186
/ GENERAL INFORMATION:
/ APPLICANT: MARASCO, Wayne A.
/ APPLICANT: SODROSKI, Joseph G.
/ APPLICANT: HASELTINE, William A.
/ APPLICANT: POSNER, Marshall R.
/ TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
/ TITLE OF INVENTION: ANTI-GP 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
/ TITLE OF INVENTION: AND USE THEREOF
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,774A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/400,674
/ FILING DATE: 08-MAR-1995
/ APPLICATION NUMBER: 07/804,652
/ FILING DATE: 10-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Resnick, David S

/
/
/ REGISTRATION NUMBER: 34,235
/ REFERENCE/DOCKET NUMBER: 41450-FWC-DIV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-523-3400
/ TELEFAX: 617-523-6440
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-480-774A-4

Query Match      79.1%; Score 583.5; DB 2; Length 129;
Best Local Similarity 89.2%; Pred. No. 4.6e-48;
Matches 116; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLLLFLLLLWLPDTTGGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLFLLLLWLPDTTGGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFF 120
DB 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFF 120

QY 121 GGGTKVEIKR 130
DB 120 GGGTKVEIKR 129

RESULT 10
US-09-456-090A-42
/ Sequence 42, Application US/09456090A
/ Patent No. 6680209
/ GENERAL INFORMATION:
/ APPLICANT: Buechler, Joe
/ APPLICANT: Valkirs, Gunars
/ APPLICANT: Gray, Jeff
/ APPLICANT: Lomberg, Nils
/ TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
/ FILE REFERENCE: 020015-000200US
/ CURRENT APPLICATION NUMBER: US/09/456,090A
/ CURRENT FILING DATE: 1999-12-06
/ NUMBER OF SEQ ID NOS: 110
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 42
/ LENGTH: 226
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION: M1-5L
/ US-09-456-090A-42

Query Match      77.9%; Score 575; DB 4; Length 226;
Best Local Similarity 90.2%; Pred. No. 5.7e-47;
Matches 111; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 21 EIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOKPGQAPRLIIYGASSRATDIP 80
DB 1 EIVMTQSPGTLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYGASSRATGIP 60

QY 81 HRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFFGGGKVEIKETVAAPSVFIF 140
DB 61 DRFSGSGSGTDFLTISRLEPEDFAVYQOQYGTSLTFFGGGKVEIKETVAAPSVFIF 120

QY 141 PPS 143
DB 121 PPS 123

RESULT 11
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US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 50
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match      77.4%; Score 571; DB 4; Length 226;
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

QY 81 HRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPYTFGGGTKLEIKRTVAAPSVFIF 120

QY 141 PPS 143
DB 121 PPS 123

RESULT 12
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match      77.4%; Score 571; DB 4; Length 226;
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

QY 81 HRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPYTFGGGTKLEIKRTVAAPSVFIF 120

QY 141 PPS 143
DB 121 PPS 123

US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 50
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match      77.4%; Score 571; DB 4; Length 226;
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

QY 81 HRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPYTFGGGTKLEIKRTVAAPSVFIF 120

QY 141 PPS 143
DB 121 PPS 123

US-09-456-090A-52
; Sequence 52, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-25L
US-09-456-090A-52

Query Match      76.8%; Score 567; DB 4; Length 224;
Best Local Similarity 91.1%; Pred. No. 3.2e-46;
Matches 112; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60
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Qy	81	HPFSGSGTDTLTISLEBEDFAVYCYQYGTSA	LTFTGGGKTVEIKETVAAPSVFIF	140
		:	:	
Db	61	HPFSGSGTDTLTISLEBEDFAVYCYQYGS	--FTFGPKTKVDIKETVAAPSVFIF	118
		:	:	
Qy	141	PPS	143	
Db	119	PPS	121	

RESULT 15

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US-09-456-090A-72
; Sequence 72, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 226
; TYPE: PRP
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-11
US-09-456-090A-72

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Query Match	76.7%	Score 566	DB 4	Length 226
Best Local Similarity	89.4%	Pred. No. 4e-46		
Matches 110	Conservative	5	Mismatches 8	Indels 0
Gaps	0			

QY	21	EIVLTFQPTLUSLFGGERATISCSASQSVASAYLANYQKPGQAPRELLIYGASSRATDIP	80
		
DB	1	EIVMTQSPGTLUSLFGGERATISCSASQSVSSYLYNYQKPGQAPRELLIYGASSRATGIP	60
		
QY	81	HFFSSGSGGTQFTLTITISLEPEDFVAVYCCQYGTSTALLTFGGGKTKVEIKRTVAAPSVFIF	140
		
DB	61	DFESSGSGGTQFTLTITISLEPEDFVAVYCCQYSGSPFFTFPGTKYDKIKRVAASQSVIF	120
		

Search completed: April 5, 2004, 13:44:09
Job time : 12.824 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 12.1827 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTRILFLVAATGTHAQ.....MTVSSASTKGPSVFPLGSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	580.5	73.7	171	2 S23623	Ig heavy chain V r
2	517.5	65.7	136	2 S31600	Ig heavy chain V r
3	513.5	65.2	135	2 S49530	anti-Sm antibody V
4	508	64.5	627	2 S14683	Ig mu chain precu
5	503	63.8	160	2 PLO105	anti-PK2 erythrocy
6	480.5	61.0	132	2 S31596	Ig heavy chain V r
7	476	60.4	148	2 S29257	Ig heavy chain V r
8	472	59.9	117	2 S18551	Ig heavy chain V r
9	469	59.5	117	2 S31680	Ig heavy chain V r
10	464	58.9	117	1 HVHU35	Ig heavy chain pre
11	455	57.7	142	2 S19245	Ig heavy chain pre
12	452	57.4	117	2 S18553	Ig heavy chain V r
13	450.5	57.2	138	2 PN0538	Ig heavy chain V r
14	449.5	57.0	143	1 ELHUND	Ig heavy chain pre
15	448	56.9	117	2 S18552	Ig heavy chain V r
16	446	56.6	117	1 HVHUHG	Ig heavy chain pre
17	446	56.6	131	2 S21924	Ig heavy chain V r
18	446	56.6	151	2 PLO011	Ig heavy chain pre
19	444	56.3	134	2 S21916	Ig heavy chain V r
20	444	56.3	142	2 A32483	Ig heavy chain V r
21	443	56.2	98	2 S26911	Ig heavy chain V r
22	440.5	55.9	469	2 S37483	Ig gamma-2a chain
23	435.5	55.3	474	1 P2M511	Ig gamma-2b chain
24	432	54.8	117	2 GT0371	Ig gamma chain pre
25	429.5	54.5	137	2 C41287	Ig heavy chain pre
26	423.5	53.7	150	2 PN0444	Ig heavy chain V r
27	422.5	53.6	475	2 S01321	Ig gamma-2b chain
28	421.5	53.5	141	2 JL0076	Ig heavy chain pre
29	420	53.3	111	2 S21925	Ig heavy chain V r

Ig heavy chain pre
Ig heavy chain V r
Ig gamma chain (WM)
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain V-1
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig gamma chain - m

ALIGNMENTS

RESULT 1

S23623
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Oleee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from C:Superfamily: immunoglobulin V region; immunoglobulin homology
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23623
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.7% Score 580.5; DB 2; Length 171;
Best Local Similarity 72.4%; Pred. No. 1.9e-41;
Matches 113; Conservative 10; Mismatches 24; Indels 9; Gaps 1;
Qy 1 MDWTRILFLVAATGTHAQVQLVQSGAEVYKFGASVKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRILFLVAATGTHAQVQLVQSGAEVYKFGASVKVSGYTLTLPVHWGQAP 60
Qy 61 GKGLVWVGSFDPESGESIYAREFGQSVMTADTSTDIAYNELSSLSRSDDTAVYVCV--- 117
Db 61 GQGLEWVGWINPNSGGTGYGQKFGQVTLFRDTSISTAYNELSRLTSDDTAVYCAIEYF 120
Qy 118 -----PDPAFDIWGQTMVTVSSASTKGPSVFPL 147
Db 121 YDGSDLKPSDFDIWGQTMVTVSSASTKGPSVFPL 156

RESULT 2

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C. Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585
A:Accession: S31600
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CU1>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 517.5; DB 2; Length 136;
Best Local Similarity 74.3%; Pred. No. 2.7e-36;
Matches 101; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAT 60

QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDP 120
DB 61 GQGLEWGMWNPNSGNTGYAQRFGVTRTNTSISTAYMELSLRSDDTAVYYCA-RWR 119

QY 121 DAFDIWGGTMTVSS 136
DB 120 DAFDIWGGTMTVSS 135

RESULT 3
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <NAH>
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA8467.1; PID:G560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 513.5; DB 2; Length 135;
Best Local Similarity 73.5%; Pred. No. 5.8e-36;
Matches 100; Conservative 11; Mismatches 24; Indels 1; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAT 60

QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDP 120
DB 61 GQGLEWGMWNPNSGNTGYAQRFGVTRTNTSISTAYMELSLRSDDTAVYYCA-RAR 119

QY 121 DAFDIWGGTMTVSS 136
DB 120 TGNYMGQGLTVSS 135

RESULT 4
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nusenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FSI>
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 508; DB 2; Length 627;
Best Local Similarity 61.2%; Pred. No. 8.5e-35;
Matches 101; Conservative 17; Mismatches 31; Indels 16; Gaps 2;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60

QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA-RAR 116
DB 61 GQGLEWGMWNPNSGNTGYAQRFGVTRTNTSISTAYMELSLRSDDTAVYYCAKTGI 120

QY 117 -----VPPDAF-----DIWGGTMTVSSASTKGPSVPLGS 149
DB 121 LGPVSSGMYNSDYVYGVMDVWGQGTITVSSGSASAPTLFPLVS 165

RESULT 5
P10105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: P10105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P10106; MUID:89235583; PMID:2541221
A:Accession: P10105
A:Molecule type: mRNA
A:Residues: 1-160 <SIL>
A:Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 63.8%; Score 503; DB 2; Length 160;
Best Local Similarity 63.4%; Pred. No. 5.2e-35;
Matches 102; Conservative 12; Mismatches 31; Indels 16; Gaps 3;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTSLPVMHWGQAP 60

QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA-VP- 118
DB 61 GQGLEWGMWNPNSGNTGYAQRFGVTRTNTSISTAYMELSLRSDDTAVYYCARPG 120

QY 119 -----DPDAFDIWGGTMTVSSASTKGPSVPLGS 149
DB 121 YCSGGGCVRGD-----DYWGQGTITVSSGSASAPTLFPLVS 157

RESULT 6
S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: Preliminary

A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 61.0%; Score 480.5; DB 2; Length 132;
Best Local Similarity 69.9%; Pred. No. 3.2e-33;
Matches 95; Conservative 11; Mismatches 25; Indels 5; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAT 60
QY 61 GKGLWVGSPDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCAVDPD 120
DB 61 GQGLEWMGNWPNPNSGNTGTAQKFGQVTRTSTISATYMELSRLSRSDDTAVYCAVDPD 116
QY 121 DAFDINGQGTMTVSS 136
DB 117 -XAPANGQGTMTVSS 131
RESULT 7
S29257
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhane, L.; van Sprosen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:92362614; PMID:1499555
A:Accession: S29257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:S42403; NID:9253699; PIDN:AA822940.1; PID:G253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 60.4%; Score 476; DB 2; Length 148;
Best Local Similarity 62.2%; Pred. No. 8.5e-33;
Matches 92; Conservative 14; Mismatches 30; Indels 12; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFAMVAHWQAP 60
QY 61 GKGLWVGSPDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCAVDPD 116
DB 61 GQGLEWMGNWISVADGKTKYKQFQEVITRTTSATTAYMEVRLSRSDDTAVYCAVDPD 116
QY 117 -----VDPDPAFDINGQGTMTVSS 136
DB 121 INMVRGLITTPPFDWQGTIVSS 148
RESULT 8
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S21625
R:Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935993
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62106; NID:G37831; PIDN:CAA44016.1; PID:G37832

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:G32552; PIDN:CAA42225.1; PID:G32553
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 59.8%; Score 472; DB 2; Length 117;
Best Local Similarity 77.6%; Pred. No. 1.4e-32;
Matches 90; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFGYNHWVRQAP 60
QY 61 GKGLWVGSPDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCA 116
DB 61 GQGLEWMGNWPNPNSGNTGTAQKFGQVTRTSTISATYMELSRLSRSDDTAVYCA 116
RESULT 9
S31680
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31680
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31680
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <CUI>
A:Cross-references: EMBL:Z14213; NID:G37795; PIDN:CAA78582.1; PID:G37796
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 59.5%; Score 469; DB 2; Length 117;
Best Local Similarity 75.9%; Pred. No. 2.5e-32;
Matches 88; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFYSYHWRQAP 60
QY 61 GKGLWVGSPDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCA 116
DB 61 GQGLEWMGNWPNPNSGNTGTAQKFGQVTRTSTISATYMELSRLSRSDDTAVYCA 116
RESULT 10
HVHU35
Ig heavy chain precursor V region (V35) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S00476; S34013
R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh
EMBO J. 7, 1047-1051, 1988
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain 1
A:Reference number: S00476; MUID:88296408; PMID:2841108

A:Accession: S00476
 A:Molecule type: DNA
 A:Residues: 1-117 <MATS>
 A:Cross-references: EMBL:X07448; NID:g33104; PIDN:CA56703.1; PID:g6002173
 A:Note: the authors translated the codon AGT for residue 89 as Met
 R:Marieette, X.; Tsapis, A.; Broquet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Reference number: S34001; MUID:93209281; PMID:7681398
 A:Accession: S34013
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 20-116 <MAR>
 C:Genetics:
 A:Gene: GDS:IGHV@
 A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 Query Match 58.9%; Score 464; DB 1; Length 117;
 Best Local Similarity 75.9%; Pred. No. 6.6e-32;
 Matches 88; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Qy 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
 Db 61 GQGLEWGWGRINPNSGGTNYAKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCA 116
 RESULT 11
 S19245
 Ig heavy chain precursor V region (10P1) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S19245
 R:Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
 EMBO J. 11, 603-609, 1992
 A:Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
 A:Reference number: S19245; MUID:92164649; PMID:1537339
 A:Accession: S19245
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-142 <KIR>
 A:Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>
 Query Match 57.7%; Score 455; DB 2; Length 142;
 Best Local Similarity 60.6%; Pred. No. 4.6e-31;
 Matches 86; Conservative 19; Mismatches 31; Indels 6; Gaps 1;
 Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Qy 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116
 Db 61 GQGLEWGWGRINPNSGGTNYAKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARAYT 120
 Qy 117 --VPDPAFDIWGGTWTVSS 136
 Db 121 LMMTAVTHDFWGGQTLTVSS 142

RESULT 12
 S18553
 Ig heavy chain V region precursor (VI-3b) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
 C:Accession: S18553; S26916
 R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Inai, T.; Yokoyama, K.; Soeda, E.;
 EMBO J. 10, 3641-3645, 1991
 A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c
 A:Reference number: S18551; MUID:92037524; PMID:1935893
 A:Accession: S18553
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-117 <SHI>
 A:Cross-references: EMBL:X62109
 R:Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26916
 A:Molecule type: DNA
 A:Residues: 20-117 <TOM>
 A:Cross-references: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 Query Match 57.4%; Score 452; DB 2; Length 117;
 Best Local Similarity 73.3%; Pred. No. 6.6e-31;
 Matches 85; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAP 60
 Qy 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
 Db 61 GQGLEWGWGRINPNSGGTNYAKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCA 116
 RESULT 13
 PNO538
 Ig heavy chain V region (clone LUNm03) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
 C:Accession: PNO538
 R:Avila, M.A.; Vazquez, J.; Danielsson, L.; de Cossio, M.E.F.; Borrebaeck, C.A.K.
 Gene 127, 273-274, 1993
 A:Title: Sequence determination of variable region genes of two human monoclonal antibo
 A:Reference number: PNO535; MUID:93273246; PMID:8500770
 A:Accession: PNO538
 A:Molecule type: DNA
 A:Residues: 1-138 <AVI>
 A:Cross-references: GB:M97804; NID:g185373; PIDN:AAB18935.1; PID:g1669777
 A:Note: the authors translated the codon CCA for residue 75 as Ser, GCC for residue 79
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 Query Match 57.2%; Score 450.5; DB 2; Length 138;
 Best Local Similarity 65.2%; Pred. No. 1.1e-30;
 Matches 90; Conservative 10; Mismatches 23; Indels 15; Gaps 1;
 Qy 20 QVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAPKGLVWVSDPDSGSIIY 79
 Db 1 QVHLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGOAPKGLVWVSDPDSGSIIY 60
 Qy 80 AREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP-----DAFD 124

```
Db 61 AQKQGRVTMTDPTDTSLELSRVSSEDVAVYCVTGPPRLSELAIFGVWKIRGPPD 120
Qy 125 IWGQGTMTVSSASTKGP 142
Db 121 IWGQGTMTVSSASTKGP 138

RESULT 14
ELHUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 05-Apr-1993 #text_change 21-Jan-2000
C:Accession: A93933; A02026
R:Kerten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: A93933
A:Molecule type: mRNA
A:Residues: 1-143 <KEN>
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Contents: annotation: partial sequence
A:Note: this epsilon chain was isolated from a myeloma protein
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F:30-113/Domain: immunoglobulin homology <IMM>
F:16/Modified site: pyroglutamic acid (Gln) (in mature form) #status experiment
F:37-111/Disulfide bonds: #status experimental

Query Match 57.0%; Score 449.5; DB 1; Length 143;
Best Local Similarity 61.2%; Pred. No. 1.3e-30;
Matches 90; Conservative 12; Mismatches 30; Indels 15; Gaps 2;

Qy 1 MDWTWRIILFLVAAATGTHAQVLQVQSGAEVKPKGASVKVCKVSGYTLTLPVHWGQAP 60
Db 1 MDWT---FLVAAATRVHSQTQLVQSGAEVKPKGASVRVCKVSGYTFIDSYIHWIRQAP 56

Qy 61 GKGLEWVGSDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDTAYVYCAVPDP 120
Db 57 GHGLEWVGWNPNSGGTNYAPRFQGRVTMTDRDASFSTAYMDLSRLSRDSDSAVFYCAKSDP 116

Qy 121 -----DAFDIWGGTMTVSS 136
Db 117 FMSDYNYFDYSYTLVDWGGTMTVSS 143

RESULT 15
S18552
Ig heavy chain V region precursor (VI-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18552
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18552
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62107; NID:g37833; PIDN:CAA44017.1; PID:g37834
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

```
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 448; DB 2; Length 117;
Best Local Similarity 73.3%; Pred. No. 1.4e-30;
Matches 85; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MDWTWRIILFLVAAATGTHAQVLQVQSGAEVKPKGASVKVCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTWRIILFLVAAATGTHAQVLQVQSGAEVKPKGASVKVCKVSGYTFISYAMHWVRQAP 60

Qy 61 GKGLEWVGSDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDTAYVYCA 116
Db 61 GORLEWVGWNSAGNGNTKYSQEFQGRVTITRDTASTAYMELSLRSDMAVYCA 116

Search completed: April 5, 2004, 13:43:01
Job time : 12.1827 secs
```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.85279 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTWRIFLVAAATGTHAQ.....MTVSSASTKGPSVFPQSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	464	58.9	117	1 HV1G HUMAN	P23083 homo sapien
2	456.5	57.9	147	1 HV1C HUMAN	P01744 homo sapien
3	446	56.6	117	1 HV1B HUMAN	P01743 homo sapien
4	414.5	52.6	139	1 HV07 MOUSE	P01751 mus musculus
5	406.5	51.6	137	1 HV11 MOUSE	P01755 mus musculus
6	396	50.3	138	1 HV48 MOUSE	P03980 mus musculus
7	374	47.5	117	1 HV05 MOUSE	P01750 mus musculus
8	374	47.5	117	1 HV09 MOUSE	P01753 mus musculus
9	373	47.3	136	1 HV15 MOUSE	P01759 mus musculus
10	369	46.8	140	1 HV02 MOUSE	P01746 mus musculus
11	364	46.2	117	1 HV04 MOUSE	P01748 mus musculus
12	360	45.7	117	1 HV49 MOUSE	P06328 mus musculus
13	356	45.2	117	1 HV14 MOUSE	P01758 mus musculus
14	355	45.1	117	1 HV10 MOUSE	P01754 mus musculus
15	354	44.9	117	1 HV05 MOUSE	P01749 mus musculus
16	351	44.5	117	1 HV1A HUMAN	P01742 homo sapien
17	350	44.4	117	1 HV52 MOUSE	P06327 mus musculus
18	346.5	44.0	118	1 HV51 MOUSE	P06330 mus musculus
19	346	43.9	117	1 HV12 MOUSE	P01756 mus musculus
20	345	43.8	117	1 HV13 MOUSE	P01757 mus musculus
21	338.5	43.0	120	1 HV50 MOUSE	P06329 mus musculus
22	332.5	42.2	114	1 HV00 MOUSE	P01741 mus musculus
23	326	41.4	120	1 HV03 MOUSE	P01747 mus musculus
24	318	40.4	121	1 HV01 MOUSE	P01745 mus musculus
25	313.5	39.8	120	1 HV1H HUMAN	P80421 homo sapien
26	313	39.7	125	1 HV1F HUMAN	P06326 homo sapien
27	306.5	38.9	122	1 HV3G HUMAN	P01768 homo sapien
28	305	38.7	121	1 HV3J HUMAN	P01771 homo sapien
29	301.5	38.3	124	1 HV1E HUMAN	P01761 homo sapien
30	293	37.2	119	1 HV3I HUMAN	P01770 homo sapien
31	291.5	37.0	136	1 HV16 MOUSE	P01783 mus musculus
32	290.5	36.9	124	1 HV1D HUMAN	P01760 homo sapien
33	290	36.8	142	1 HV01 RAT	P01805 rattus norv

34	286.5	36.4	114	1 HV01 CANFA	P01784 canis famil
35	284.5	36.1	122	1 HV3H HUMAN	P01769 homo sapien
36	284	36.0	119	1 HV3L HUMAN	P01773 homo sapien
37	280.5	35.6	117	1 HV03 CARAU	P19180 carassius a
38	277.5	35.2	120	1 HV3U HUMAN	P01782 homo sapien
39	276	35.0	117	1 HV3C HUMAN	P01764 homo sapien
40	275	34.9	115	1 HV3D HUMAN	P01765 homo sapien
41	274.5	34.8	114	1 HV3B HUMAN	P01783 homo sapien
42	274.5	34.8	116	1 HV3T HUMAN	P01772 homo sapien
43	272.5	34.6	126	1 HV3K HUMAN	P01772 homo sapien
44	272	34.5	117	1 HV01 CAICR	P01813 caiman croc
45	271.5	34.5	119	1 HV38 MOUSE	P01808 mus musculu

ALIGNMENTS

RESULT 1

HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin heavy-chain locus.";
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC
CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVHU35.
DR HSRP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 58.9%; Score 464; DB 1; Length 117;
Best Local Similarity 75.9%; Pred. No. 1.5e-36;
Matches 88; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEYKPKGASVKVSGYGLTLPVHWVQAP 60
DB 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEYKPKGASVKVSGYGLTLPVHWVQAP 60

Qy 61 GKLEWVSGDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
 Db 61 GQGLEWNGRINPNSGGTNYAKQFQGRVTSPTDTSISTAYMELSLRSDDTAVYYCA 116

RESULT 2

HVIC_HUMAN STANDARD; PRT; 147 AA.
 AC P01744;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region ND precursor (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RZ SEQUENCE FROM N.A.

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 CC [2]
 CC SEQUENCE OF 20-147.

RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RL (In) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).

CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP: P01789; IMCP
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR SMART; SMO0406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal; Pyroliidone carboxylic acid.

FT CHAIN 1
 FT SIGNAL 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
 FT DOMAIN 20 131 IG-LIKE.

FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 41 115
 FT CONFLICT 21 21 T -> V (IN REF. 2).
 FT CONFLICT 53 54 IH -> HI (IN REF. 2).
 FT CONFLICT 67 68 VG -> GV (IN REF. 2).
 FT CONFLICT 125 125 MISSING (IN REF. 2).
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16491 MW; 9489F72A5366C20 CRC64;

Query Match 57.9%; Score 456.5; DB 1; Length 147;
 Best Local Similarity 61.2%; Pred. No. 9.6e-36;
 Matches 90; Conservative 12; Mismatches 34; Indels 11; Gaps 1;

Qy 1 MDWTRILFLVAAATGTHAQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWVQAP 60
 Db 1 MDWTRVFLVAAATRVHSGTQLVQSGAEVKPGASVRVSKASGYTFIDSYHWIRQAP 60

Qy 61 GKLEWVSGDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDP 120
 Db 61 GHGLEWGVINPNSGGTNYAPRPGRVITMDTASFTAYMDLSRSDSDSAVFYCAKSP 120

Qy 121 -----DAFDINGQGTMTVSS 136

Db 121 FWSDYNFDSYTLVDVWGQGTMTVSS 147

RESULT 3

HVIC_HUMAN STANDARD; PRT; 117 AA.
 AC P01743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region HG3 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RA MEDLINE=83144028; PubMed=6298778;
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region
 RT (VH) gene subgroups."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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EMBL; J00240; AAA52988.1; -.
 DR PIR; A02024; HVH0HG.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SMO0406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.

KW SIGNAL 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
 FT DOMAIN 20 >117 IG-LIKE.

FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 56.6%; Score 446; DB 1; Length 117;
 Best Local Similarity 70.7%; Pred. No. 7.1e-35;
 Matches 82; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MDWTRILFLVAAATGTHAQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWVQAP 60
 Db 1 MDWTRVFLVAAATRVHSGTQLVQSGAEVKPGASVRVSKASGYTFIDSYHWIRQAP 60
 Qy 61 GKLEWVSGDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
 Db 61 GQGLEWNGIINPNSGGTNYAKQFQGRVITMDTSTSTVYMLSLRSDDTAVYYCA 116

RESULT 4

HVIC_HUMAN STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RZ SEQUENCE FROM N.A.

```

RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00529; AAA38170.1; -
CC PIR: A02038; GMS43.
CC FDB: 1A6W; 27-MAY-98.
CC PDB: 1A6W; 15-JUL-98.
CC InterPro: IPR007110; IG-like.
CC SMART: SM00406; IG; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 62 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 139 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 52.6%; Score 414.5; DB 1; Length 139;
Best Local Similarity 57.6%; Pred. No. 7.5e-32;
Matches 80; Conservative 17; Mismatches 39; Indels 3; Gaps 1;

QY 1 MDWTWRIILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWVGQAP 60
Db 1 MGWSCIMFLAATATGTVHSGVQLQPGAEIYKPGASVKLSCKASGYTFTSYMHWVQRP 60
QY 61 GKGLWVGSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCAVPD- 119
Db 61 GRGLEWIGRIDPNSGGTKYNEFKSKATLTVDKPSSTAYMQLSLTSDSAVYVCARYDY 120
QY 120 --PDADFIDWGQGTMTVSS 136
Db 121 YGSSYFDYWGQGTTLTVSS 139

RESULT 5
HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00539; AAA38172.1; -
CC PIR: A02038; GMS43.
CC HSP: P01810; 2FBJ.
CC InterPro: IPR007110; IG-like.
CC SMART: SM00406; IG; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 62 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 137 137
CC SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 51.6%; Score 406.5; DB 1; Length 137;
Best Local Similarity 57.7%; Pred. No. 4.1e-31;
Matches 79; Conservative 15; Mismatches 42; Indels 1; Gaps 1;

QY 1 MDWTWRIILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWVGQAP 60
Db 1 MGWSCIMFLAATATGTVHSGVQLQPGAEIYKPGASVKLSCKASGYTFTSYLMMHWVQRP 60
QY 61 GKGLWVGSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYCA-VPD 119
Db 61 GRGLEWIGRIDPNSGGTKYNEHFRSKATLTIDKPSSTAYMQLSLTSDSAVYVCARYL 120
QY 120 PDADFIDWGQGTMTVSS 136
Db 121 GRYFDYWGQGTTLTVSS 137

RESULT 6
HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 13-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F.,

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RA Tucker P.W.:
RT "Illegitimate recombination generates a class switch from C mu to C
RL delta in an Igd-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMS17.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 74815734C6907B8E CRC64;

Query Match 50.3%; Score 396; DB 1; Length 138;
Best Local Similarity 55.1%; Pred. No. 4e-30;
Matches 76; Conservative 20; Mismatches 40; Indels 2; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGVYTLTLPVHWGQAP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MGWSYILFLVATVDVHSQVQLQPGAEVKGASVQLCKASGHTFTNYHWVKQRP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GKGLWVGSFDPSSGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVPP 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 GQGLEWIGEINPDGRSNYNEKFKATLTVDKSSSTAYMQLSSLTPEEFAYVYCARSDG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 --DAFDWGQGTVMTVSS 136
DB 121 YDWFVYWGQGLTVTSA 138

RESULT 7
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; D90809; HVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.5%; Score 374; DB 1; Length 117;
Best Local Similarity 59.5%; Pred. No. 3.7e-28;
Matches 69; Conservative 16; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGVYTLTLPVHWGQAP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MGWSYILFLVATVDVHSQVQLQPGAEVKGASVQLCKASGHTFTNYHWVKQRP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GKGLWVGSFDPSSGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAV 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 GQGLEWIGRIHPSDSDTNQKFKATLTVDKSSSTAYMQLSSLTSEDSAVYCAI 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; D90809; HVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.5%; Score 374; DB 1; Length 117;
Best Local Similarity 59.5%; Pred. No. 3.7e-28;
Matches 69; Conservative 16; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGVYTLTLPVHWGQAP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MGWSYILFLVATVDVHSQVQLQPGAEVKGASVQLCKASGHTFTNYHWVKQRP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GKGLWVGSFDPSSGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAV 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 GQGLEWIGRIHPSDSDTNQKFKATLTVDKSSSTAYMQLSSLTSEDSAVYCAI 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVM523.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 46.28; Score 364; DB 1; Length 117;
Best Local Similarity 58.63; Pred. No. 3.2e-27;
Matches 68; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MDWTWRIILFLVAATGTHAQVQVQSGAEVVKFGASVKVSGYTLTLPVHWYQAP 60
DB 1 MGWSCIIILFLVAANGVHSVQLQPGTELKVGASVKLSCKASGYTFTSYNHWYKQRP 60
QY 61 GKLEWVGSDPPSGESYIAREFQGSVTMTADTSTDIAYMELSLSDTAVYCA 116
DB 61 GQGLEWIGNPFGNGTNYNEKPKSKATLVDRKPSSTAYTQLSLTSSEDSAVYCA 116

RESULT 12
HV49 MOUSE
ID HV49 MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13786; AAA38506.1; --
CC PIR; A02035; MHMSB4.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.

QY 1 MDWTWRIILFLVAATGTHAQVQVQSGAEVVKFGASVKVSGYTLTLPVHWYQAP 60
DB 1 MGWSCIIILFLVAANGVHSVQLQPGTELKVGASVKLSCKASGYTFTSYNHWYKQRP 60
QY 61 GKLEWVGSDPPSGESYIAREFQGSVTMTADTSTDIAYMELSLSDTAVYCA 116
DB 61 GQGLEWIGNPFGNGTNYNEKPKSKATLVDRKPSSTAYTQLSLTSSEDSAVYCA 116

RESULT 13
HV14 MOUSE
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00488; AAA38519.1; --
CC PIR; A02041; HVM58A.
CC HSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 45.74; Score 360; DB 1; Length 117;
Best Local Similarity 57.44; Pred. No. 7.6e-27;
Matches 66; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDWTWRIILFLVAATGTHAQVQVQSGAEVVKFGASVKVSGYTLTLPVHWYQAP 60
DB 1 MGWSCIIILFLVAATGTHAQVQVQSGAEVVKFGASVKVSGYTLTLPVHWYQAP 60
QY 61 GKLEWVGSDPPSGESYIAREFQGSVTMTADTSTDIAYMELSLSDTAVYCA 115
DB 61 GRGLEWIGNIDPNSGGTKYNEKPKSKATLVDRKPSSTAYTQLSLTSSEDSAVYCA 115

RESULT 13
HV14 MOUSE
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00488; AAA38519.1; --
CC PIR; A02041; HVM58A.
CC HSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

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Query Match 45.2%; Score 356; DB 1; Length 117;
Best Local Similarity 55.4%; Pred. No. 1.8e-26;
Matches 64; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MDWTWRLFLVAAATGTHAQLVQSGAEVKKPGASVKVSCKVSGYVLTLPVHWVQGP 60
Db 1 MGWSWIFLLSCTAGVSHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWVQKH 60

Qy 61 GKLEWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLSRDSTAVYCA 116
Db 61 GKLEWIGIYIPYNGGTGYNQKPKATLTVDNSSSTAYMELSSLTSEDSAVYCA 116

RESULT 14
HV10 MOUSE
ID HV10 MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
DR EMBL; J00533; AAA38602.1; -
DR PIR; C90809; HVNS45.
DR HSP; P01810; 2PBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON TER 117
FT SEQUENCE 117 AA; D37D58A3F543E996 CRC64;
SQ
Query Match 45.1%; Score 355; DB 1; Length 117;
Best Local Similarity 57.8%; Pred. No. 2.2e-26;
Matches 67; Conservative 15; Mismatches 34; Indels 0; Gaps 0;

Qy 1 MDWTWRLFLVAAATGTHAQLVQSGAEVKKPGASVKVSCKVSGYVLTLPVHWVQGP 60
Db 1 MGWSWIFLLSCTAGVSHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWVQKH 60

Qy 61 GKLEWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLSRDSTAVYCA 116
Db 61 GKLEWIGIYIPYNGGTGYNQKPKATLTVDNSSSTAYMELSSLTSEDSAVYCA 116

RESULT 15
HV05 MOUSE
ID HV05 MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVNS3.
DR HSP; P01810; 2PBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
FT SEQUENCE 117 AA; 427C861C53975EDC CRC64;
SQ
Query Match 44.9%; Score 354; DB 1; Length 117;
Best Local Similarity 56.9%; Pred. No. 2.7e-26;
Matches 66; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MDWTWRLFLVAAATGTHAQLVQSGAEVKKPGASVKVSCKVSGYVLTLPVHWVQGP 60
Db 1 MGWSWIFLLVATATGTHAQLVQSGAEVKKPGASVKVSCKASGYTFTSWMDVWVQRP 60

Qy 61 GKLEWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLSRDSTAVYCA 116
Db 61 GQGLEWIGNIYPSDSETHYQKFKDKATLTVDKSSSTAYMQLSLTSEDSAVYCA 116
```

Search completed: April 5, 2004, 13:24:55
Job time : 7.85279 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 31.9797 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTRILFLVAARTGTHAQ.....MTVSSASTKGPSVFPLGSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 4: sp.human:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.organella:*
 - 9: sp.phage:*
 - 10: sp.plant:*
 - 11: sp.rodent:*
 - 12: sp.virus:*
 - 13: sp.vertibrate:*
 - 14: sp.unclassified:*
 - 15: sp.rvirus:*
 - 16: sp.bacteriap:*
 - 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788	100.0	150	4 Q9Y298	Q9Y298 homo sapien
2	520.5	66.1	469	4 Q7Z7P5	Q7Z7P5 homo sapien
3	510	64.7	614	4 Q9SGA6	Q9SGA6 homo sapien
4	478.5	60.7	500	4 Q9BRV0	Q9BRV0 homo sapien
5	467	59.3	497	4 Q8WY24	Q8WY24 homo sapien
6	466	59.1	473	11 Q9D8L4	Q9D8L4 mus musculus
7	464	58.9	157	4 Q9S978	Q9S978 homo sapien
8	461.5	58.6	159	4 Q9EQS0	Q9EQS0 homo sapien
9	445.5	56.5	613	11 Q8VCX7	Q8VCX7 mus musculus
10	445	56.5	168	11 Q8VDC9	Q8VDC9 mus musculus
11	445	56.5	484	11 Q9JLA6	Q9JLA6 mus musculus
12	443.5	56.3	482	11 Q8K172	Q8K172 mus musculus
13	435.5	55.3	278	11 Q921K1	Q921K1 mus musculus
14	434.5	55.1	463	11 Q99LQ4	Q99LQ4 mus musculus
15	431.5	54.8	473	11 Q99L25	Q99L25 mus musculus
16	429	54.4	470	11 Q7TMK1	Q7TMK1 mus musculus

17	428	54.3	468	11 Q99L31	Q99L31 mus musculus
18	425	53.9	125	4 Q9UL95	Q9UL95 homo sapien
19	421.5	53.5	124	4 Q9UL92	Q9UL92 homo sapien
20	421	53.4	480	11 Q8K0Z4	Q8K0Z4 mus musculus
21	421	53.4	481	11 Q91WT1	Q91WT1 mus musculus
22	418.5	53.1	488	11 Q91WR1	Q91WR1 mus musculus
23	412.5	52.3	496	4 Q96DK0	Q96DK0 homo sapien
24	409.5	52.0	481	11 Q8VCV5	Q8VCV5 mus musculus
25	409.5	52.0	488	11 Q8K0F2	Q8K0F2 mus musculus
26	409	51.9	474	11 Q833H6	Q833H6 mus musculus
27	407	51.6	119	4 Q9UL94	Q9UL94 homo sapien
28	407	51.6	614	11 Q7TMT6	Q7TMT6 mus musculus
29	406	51.5	481	11 Q91WT3	Q91WT3 mus musculus
30	405	51.4	489	11 Q8VCX4	Q8VCX4 mus musculus
31	398.5	50.6	143	11 Q924R0	Q924R0 mus musculus
32	398.5	50.6	145	11 Q924R4	Q924R4 mus musculus
33	394.5	50.1	145	11 Q924R1	Q924R1 mus musculus
34	393.5	49.9	143	11 Q924Q5	Q924Q5 mus musculus
35	392.5	49.8	143	11 Q91VA2	Q91VA2 mus musculus
36	392.5	49.8	143	11 Q924R7	Q924R7 mus musculus
37	391	49.6	142	11 Q924Q1	Q924Q1 mus musculus
38	390.5	49.6	143	11 Q91V67	Q91V67 mus musculus
39	390.5	49.6	145	11 Q924P7	Q924P7 mus musculus
40	388.5	49.3	145	11 Q924Q9	Q924Q9 mus musculus
41	388.5	49.3	145	11 Q924Q7	Q924Q7 mus musculus
42	388	49.2	146	11 Q924Q3	Q924Q3 mus musculus
43	387.5	49.2	145	11 Q924R3	Q924R3 mus musculus
44	386.5	49.0	145	11 Q924Q6	Q924Q6 mus musculus
45	385.5	48.9	137	11 Q924R6	Q924R6 mus musculus

ALIGNMENTS

RESULT 1

Q9Y298 PRELIMINARY; PRT; 150 AA.
ID AC Q9Y298
DC Q9Y298; 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IGG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; P:immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL.
FT NON_TER
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
Query Match 100.0%; Score 788; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.9e-66;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
Db 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
QY 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
Db 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
QY 121 DAFDINGQGTMTVSSASTKGPSVFPPLGS 150
Db 121 DAFDINGQGTMTVSSASTKGPSVFPPLGS 150

RESULT 2
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spine;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHarac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 64.7%; Score 510; DB 4; Length 614;
Best Local Similarity 66.0%; Pred. No. 3.6e-39;
Matches 101; Conservative 17; Mismatches 31; Indels 4; Gaps 1;

QY 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
Db 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
QY 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 116
Db 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
QY 117 VPDPAFDINGQGTMTVSSASTKGPSVFPPLGS 149
Db 121 SSMDDAFDINGQGTMTVSSASTKGPSVFPPLGS 153

RESULT 4
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
```

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Db 121 GOVGFDPDSMGQGTMTVSSASTKGPSVFPPL 150

RESULT 3
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHarac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 64.7%; Score 510; DB 4; Length 614;
Best Local Similarity 66.0%; Pred. No. 3.6e-39;
Matches 101; Conservative 17; Mismatches 31; Indels 4; Gaps 1;

QY 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
Db 1 MDWTWILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWGQAP 60
QY 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 116
Db 61 GKGLWVGSPDPSGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
QY 117 VPDPAFDINGQGTMTVSSASTKGPSVFPPLGS 149
Db 121 SSMDDAFDINGQGTMTVSSASTKGPSVFPPLGS 153

RESULT 4
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 60.7%; Score 478.5; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 2.5e-36;
Matches 96; Conservative 13; Mismatches 38; Indels 11; Gaps 2;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCA--- 116
DB 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCA--- 116
QY 117 ---VPDPAF-----DIWGGTQMTVTSASSTKGPSVPL 147
DB 121 SYSSCNDYVYMYDMVWGKTTVTSSASPTSPKVPL 158

RESULT 5
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RA "Identification and characterization of SNC66, a Ig-like gene which is
RA down-regulated in colorectal cancer."
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL: AF283666; AAL36987.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 59.3%; Score 467; DB 4; Length 497;
Best Local Similarity 57.4%; Pred. No. 2.9e-35;
Matches 89; Conservative 24; Mismatches 34; Indels 8; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVDP- 119
DB 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVDP- 119
QY 120 -----PDADFDTWGGTQMTVTSASSTKGPSVPL 147
DB 121 RGRGFGYWNFDPWGHTLVTSASPTSPKVPL 155

RESULT 6

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Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE I81060009R1k protein.
GN IGH-1 OR I81060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringuwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Yushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1; -.
DR PIR: S26746; S26746.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 59.1%; Score 466; DB 11; Length 473;
Best Local Similarity 57.7%; Pred. No. 3.4e-35;
Matches 86; Conservative 23; Mismatches 38; Indels 2; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
DB 1 MEWSWVFLLSVTAGVHCQVQLKQSGAEVKKVQSGVKVSGYTLTLPVHWGQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVP-- 118
DB 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVP-- 118
QY 119 DPADFDTWGGTQMTVTSASSTKGPSVPL 147
DB 121 DYDFAYWGGTGLTVSAKTAPSVYPL 149

RESULT 7
Q95978 PRELIMINARY; PRT; 157 AA.
AC Q95978;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembi P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416332, CAC94867.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match          56.5%; Score 445; DB 11; Length 168;
Best Local Similarity 55.7%; Pred. No. 8.3e-34;
Matches 83; Conservative 21; Mismatches 43; Indels 2; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
Db 1 MEWTWFLFLSVTAGVHSQVQLQCGAELMKPGASVKCKATGTFSSYIDWYKQRP 60

QY 61 GKGLWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GHGLEWIGELPGSGRTNYNEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYYCANYGS 120

QY 121 DA--FDIWGGTWMVTVSSASTKGPSVPL 147
Db 121 SRMYFDVWGAGTIVTSSTKTTPSVYPL 149

RESULT 11
Q99LA6 PRELIMINARY; PRT; 484 AA.
AC -Q99LA6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034395; AA03495.1; -.
DR PIR; F33932; F33932.
DR HSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 484 AA; 52567 MW; 8BAEA4F9BCF582FA CRC64;

Query Match          56.5%; Score 445; DB 11; Length 484;
Best Local Similarity 52.3%; Pred. No. 3.2e-33;
Matches 79; Conservative 31; Mismatches 37; Indels 4; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
Db 1 MEWTWFLFLSVTAGVHSQVQLQCGAELMKPGASVKCKATGTFSSYIDWYKQRP 60

QY 61 GKGLWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GHGLEWIGELPGSGRTNYNEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYYCANYGS 120

QY 121 DA--FDIWGGTWMVTVSSASTKGPSVPL 147
Db 121 SRMYFDVWGAGTIVTSSTKTTPSVYPL 149

RESULT 12
Q8KL72 PRELIMINARY; PRT; 482 AA.
ID Q8KL72;
AC Q8KL72;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to expressed sequence AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AA02849.1; -.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match          56.3%; Score 443.5; DB 11; Length 482;
Best Local Similarity 56.8%; Pred. No. 4.4e-33;
Matches 84; Conservative 20; Mismatches 43; Indels 1; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIMFLAATATGHSQVQLQCGAELVKPGASVKLSCKASGYTFTSTWMEHWKQRP 60

QY 61 GKGLWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 119
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTREGD 120

QY 120 PDAPFWGQGTWMVTVSSASTKGPSVPL 147
Db 120 PDAPFWGQGTWMVTVSSASTKGPSVPL 147

```



```
Db 121 YDAMYWGQCTSVTSSEPARPTIYPL 148
      121 YDAMYWGQCTSVTSSEPARPTIYPL 148

RESULT 13
Q921KI PRELIMINARY; PRT; 278 AA.
ID Q921KI
AC Q921KI
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
KW SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 55.3%; Score 435.5; DB 11; Length 278;
Best Local Similarity 56.7%; Pred. No. 1.2e-32;
Matches 85; Conservative 18; Mismatches 44; Indels 3; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWVQAP 60
Db 1 MGWNCIILFVATATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWVQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP-- 118
Db 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP-- 118
QY 119 -DPAFINGQGTMTVSSASTKGPSVFPL 147
Db 121 YDDYFVFWGAGTMTVSSAKTTPSVYPL 150

RESULT 14
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4
AC Q99LC4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181006O009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR F1R; B45837; B45837.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.

SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 55.1%; Score 434.5; DB 11; Length 463;
Best Local Similarity 54.0%; Pred. No. 2.9e-32;
Matches 81; Conservative 25; Mismatches 41; Indels 3; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWVQAP 60
Db 1 MEWVIFLFLSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFYTGVSQVWVQRT 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
Db 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
QY 121 DAFDI---WGQGTMTVTVSSASTKGPSVFPL 147
Db 121 YSYDLFAFWGQGTMTVTVSSAAKTPPSVYPL 150

RESULT 15
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181006O009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 54.8%; Score 431.5; DB 11; Length 473;
Best Local Similarity 52.6%; Pred. No. 5.8e-32;
Matches 81; Conservative 24; Mismatches 42; Indels 7; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWVQAP 60
Db 1 MEWSVFLFLLSVTTGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTFDTTHWVKQRP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
Db 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
QY 121 -----DAFDWGQGTMTVTVSSASTKGPSVFPL 147
Db 121 IYGVGLYFDYWGQGTMTVTVSSAKTTPSVYPL 154

Search completed: April 5, 2004, 13:42:03
Job time : 34.9797 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:09:21 ; Search time 48.4772 Seconds

(without alignments)
874.270 Million cell updates/sec

Title: US-10-044-569B-2

Perfect score: 788

Sequence: 1 MOWTWRIFLVAAATGTHAQ.....MVTSSASTKQPSVFPGLGR 150

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	100.0	150	4	AAB47058 Heavy cha
2	788	100.0	150	5	AAO18876 Human B02
3	645.5	81.9	535	4	AAAM1145 Human pol
4	627.5	79.6	146	2	AAV24372 Human mon
5	625.5	79.4	146	2	AAV24371 Human mon
6	617	78.3	528	4	AAW39359 Human pol
7	590	74.9	470	5	AAU74236 Anti-huma
8	580.5	73.7	471	7	ADE28427 Human ant
9	563.5	71.5	467	4	AAAB36210 Human imm
10	545.5	69.2	219	3	AAV96302 Human IGF
11	539	68.4	476	2	AAW88464 Monoclon
12	536	68.0	652	2	AAW48650 Heavy cha
13	535.5	68.0	249	2	AAV77610 Humanised
14	535	67.9	117	2	AAE66316 Human imm
15	532	67.5	476	6	ABU08022 Monoclon
16	526.5	66.8	249	2	AAV77615 Humanised
17	525	66.6	120	4	AAAM39164 Human pol
18	525	66.6	470	3	AAW90935 Humanised
19	525	66.6	470	3	AAW90933 Humanised
20	525	66.6	470	5	ABB74904 Mouse hum
21	525	66.6	470	5	ABB74902 Humanised
22	524	66.5	470	3	AAW90934 Humanised
23	524	66.5	470	5	ABB74903 Mouse hum
24	523	66.4	470	3	AAW90936 Humanised
25	523	66.4	470	5	ABB74945 Humanised

26	522.5	66.3	236	4	AAB36215	Aab36215 Human imm
27	522	66.2	470	2	AAW83037	Aaw83037 Anti-Pas
28	522	66.2	470	3	ABAB14779	Abab14779 Humanised
29	522	66.2	470	3	AAW90929	Aaw90929 Humanised
30	522	66.2	470	5	ABB74944	Abb74944 Humanised
31	522	66.2	470	5	ABB74898	Abb74898 Humanised
32	521.5	66.2	197	5	ABP43131	Abp43131 Human Ova
33	519.5	65.9	481	2	AAAR24442	Aar24442 Sequence
34	518.5	65.8	515	4	AAAM52162	Aam52162 Humanised
35	518.5	65.8	517	4	AAAM52154	Aam52154 Humanised
36	518.5	65.8	519	4	AAAM52165	Aam52165 Humanised
37	518.5	65.8	519	4	AAAM52164	Aam52164 Humanised
38	518.5	65.8	521	4	AAAM52163	Aam52163 Humanised
39	518.5	65.8	525	4	AAAM52166	Aam52166 Humanised
40	518.5	65.8	527	4	AAAM52155	Aam52155 Humanised
41	518.5	65.8	529	4	AAAM52168	Aam52168 Humanised
42	518.5	65.8	531	4	AAAM52167	Aam52167 Humanised
43	518.5	65.8	729	4	AAAM52158	Aam52158 Humanised
44	518.5	65.8	730	4	AAAM52157	Aam52157 Humanised
45	518.5	65.8	731	4	AAAM52156	Aam52156 Humanised

ALIGNMENTS

RESULT 1

AAB47058
ID AAB47058 standard; protein; 150 AA.

XX AC AAB47058;

XX DT 08-MAY-2001 (first entry)

XX DE Heavy chain variable region VH of BO2C11.

XX KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;
KW complementarity determining region; CDR; MAB; BO2C11;
KW conformational epitope; factor VIII; KR1X1; von Willebrand factor;
KW hemostasis; intravascular coagulation; arterial thrombosis;
KW arterial restenosis; venous thrombosis; arteriosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 44..53

FT Domain /label= CDR1

FT Domain 68..86

FT Domain /label= CDR2

FT Domain 115..125

FT Domain /label= CDR3

XX WO200104269-A1.

XX 18-JAN-2001.

XX 13-JUL-2000; 2000WO-EP006677.

XX 14-JUL-1999; 99GB-00016450.

XX 14-JUL-1999; 99US-0143891P.

XX (LEUV-) LEUVEN RES & DEV VZW.

XX Jacquemin MG, Saint-Remy JR;

XX WPI; 2001-138333/14.

XX N-PSDB; AAC85451.

XX Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.

XX Example 5; Fig 6; 55pp; English.

CC This sequence represents the heavy chain variable region of the human
 CC monoclonal antibody (MAB), B02C11. B02C11 is a human MAB which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg2150His factor
 CC VIII light chains. The MAB produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X 1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC hemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 XX

XX Sequence 150 AA;

Query Match 100.0%; Score 788; DB 4; Length 150;
 Best Local Similarity 100.0%; Pred. No. 8.1e-61;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
 DB 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
 QY 61 GKLEWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 DB 61 GKLEWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 QY 121 DAFDINGQGTMTVTVSSASTKGPSVFPLGSR 150
 DB 121 DAFDINGQGTMTVTVSSASTKGPSVFPLGSR 150

RESULT 2

AAO18876
 ID AAO18876 standard; protein; 150 AA.

AC AAO18876;

DT 07-NOV-2002 (first entry)

XX Human B02C11 heavy chain variable region.

XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antiinflammatory.

XX Homo sapiens.

Key Location/Qualifiers
 FT Region 44..53
 FT /label= CDR1
 FT Region 68..86
 FT /label= CDR2
 FT Region 115..125
 FT /label= CDR3

XX EPI222929-A2.

XX 17-JUL-2002.

XX 11-JAN-2002; 2002EP-00447005.

XX 11-JAN-2001; 2001US-0261405P.

XX (COLL-) COLLEN RES FOUND VZW D.

XX Jacquemin MG, Saint-Remy JR;

XX

XX WPI; 2002-610270/66.
 DR N-PSDB; AAL49254.

XX Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.

XX Disclosure; Fig 10; 41pp; English.

XX The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the heavy chain variable region of B02C11

XX Sequence 150 AA;

Query Match 100.0%; Score 788; DB 5; Length 150;
 Best Local Similarity 100.0%; Pred. No. 8.1e-61;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
 DB 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
 QY 61 GKLEWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 DB 61 GKLEWVGSPDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 QY 121 DAFDINGQGTMTVTVSSASTKGPSVFPLGSR 150
 DB 121 DAFDINGQGTMTVTVSSASTKGPSVFPLGSR 150

RESULT 3

AAO41145

ID AAO41145 standard; protein; 535 AA.

AC AAO41145;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6076.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

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PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AA160301.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 6076; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA158442-AA162213) with neurotropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 535 AA;
SQ
Query Match 81.9%; Score 645.5; DB 4; Length 535;
Best Local Similarity 84.5%; Pred. No. 8.2e-48;
Matches 125; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWVQAP 60
DB 15 MDCTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWVQAP 74
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
DB 75 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCATDGH 134
QY 121 D-AFDIWGQGTMTVSSASTKGPSVPFL 147
DB 135 DYAFDIWGQGTMTVSSASTKGPSVPFL 162
RESULT 4
AA124372
ID AAY24372 standard; protein; 146 AA.
XX
XX AAY24372;
XX
XX 17-SEP-1999 (first entry)
XX
XX Human monoclonal antibody against CTGF SEQ ID NO:12.
XX
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
XX cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
XX skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
XX rheumatic vascular inflammation.
XX
XX Homo sapiens.
XX
XX WO9933878-A1.
XX
XX 08-JUL-1999.
XX
XX 16-DEC-1998; 98WO-JP005697.
XX
XX 25-DEC-1997; 97JP-00367699.
XX
XX 15-DEC-1998; 98JP-00356183.
XX
XX (N1SB ) JAPAN TOBACCO INC.
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
XX
XX WPI: 1999-430232/36.
XX
XX N-PSDB; AAX90022.
DR

```

```

PR 15-DEC-1998; 98JP-00356183.
XX
XX (N1SB ) JAPAN TOBACCO INC.
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
XX
XX WPI: 1999-430232/36.
XX
XX N-PSDB; AAX90023.
XX
XX New monoclonal antibody reactive with connective tissue growth factor
PT useful in the treatment of cell proliferation disorders.
XX
XX Claim 17; Page 184-185; 212pp; Japanese.
XX
XX AAX90020 to AAX90029 encode monoclonal antibodies which react with human
CC connective tissue growth factor (CTGF). AAY24369 to AAY24378 represent
CC these monoclonal antibodies. The antibodies are useful in the diagnosis,
CC prevention and treatment of cell proliferation disorders in which CTGF is
CC implicated, including fibrosis of lung, kidney, liver and other tissues;
CC liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis;
CC rheumatic vascular inflammation; hepatitis; and cancer
XX
XX Sequence 146 AA;
SQ
Query Match 79.6%; Score 627.5; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 7.1e-47;
Matches 123; Conservative 7; Mismatches 13; Indels 3; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWVQAP 60
DB 1 MDCTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWVQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCA---V 117
DB 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCATSTV 120
QY 118 PDPADFIDWGQGTMTVSSASTKGPS 143
DB 121 VTPWFIDWGQGTMTVSSASTKGPS 146
RESULT 5
AA124371
ID AAY24371 standard; protein; 146 AA.
XX
XX AAY24371;
XX
XX 17-SEP-1999 (first entry)
XX
XX Human monoclonal antibody against CTGF SEQ ID NO:10.
XX
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
XX cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
XX skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
XX rheumatic vascular inflammation.
XX
XX Homo sapiens.
XX
XX WO9933878-A1.
XX
XX 08-JUL-1999.
XX
XX 16-DEC-1998; 98WO-JP005697.
XX
XX 25-DEC-1997; 97JP-00367699.
XX
XX 15-DEC-1998; 98JP-00356183.
XX
XX (N1SB ) JAPAN TOBACCO INC.
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
XX
XX WPI: 1999-430232/36.
XX
XX N-PSDB; AAX90022.
DR

```



```
PR 18-MAY-2000; 2000JP-00147116.
PR 30-MAR-2001; 2001JP-00099508.
XX
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX Tsuji T, Tezuka K, Hori N;
XX
XX WPI; 2002-075313/10.
XX N-PSDB; AAS99472.
XX
XX New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
XX Claim 30; Page 264-266; 300pp; English.
XX
XX The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AIIIM, for modulating proliferation
CC of AIIIM-expressing cells, for modulating production of a cytokine from
CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AIIIM-expressing cells and/or immune cytolysis or apoptosis of
CC AIIIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AIIIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
CC AIIIM monoclonal antibody amino acid sequences of the invention
XX
XX Sequence 470 AA;
XX
XX Query Match 74.9%; Score 590; DB 5; Length 470;
XX Best Local Similarity 75.5%; Pred. No. 4.7e-43;
XX Matches 11; Conservative 8; Mismatches 22; Indels 8; Gaps 1;
XX
XX QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVGYTLTSLPVMHWQAP 60
XX Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVGYTLTSLPVMHWQAP 60
XX
XX QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP 118
XX Db 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP 118
XX
XX QY 61 GQGLEWGWINPHSGGNTYAKQFGGRVTMTDTSISTAYMELSLRSDDTAVYCAVP 120
XX Db 61 GQGLEWGWINPHSGGNTYAKQFGGRVTMTDTSISTAYMELSLRSDDTAVYCAVP 120
XX
XX QY 119 -----DPDAFDIWGGQGTMTVSSASTKGPSVFPPL 147
XX Db 121 YDSSGYHDAFDIWGGQGTMTVSSASTKGPSVFPPL 155
XX
XX RESULT 8
XX ADE28427
XX ID ADE28427 standard; protein; 471 AA.
XX
XX AC ADE28427;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
XX
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX human; variable region heavy chain; 21-2-1.
XX
```

```
XX Homo sapiens.
XX OS WO2003040170-A2.
XX PN 15-MAY-2003.
XX PD
XX PF 08-NOV-2002; 2002WO-US036107.
XX PR 09-NOV-2001; 2001US-0348980P.
XX PA (PFIZ ) PFIZER PROD INC.
XX PA (ABGE-) ABGENIX INC.
XX
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
XX WPI; 2003-441521/41.
XX N-PSDB; ADE28426.
XX
XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
XX Claim 1; SEQ ID NO 34; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
XX its antigen-binding portion that specifically binds to and activates
XX human CD40. The anti-CD40 antibody of the invention demonstrates
XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX activities and may be useful for treating a hyperproliferative disorder
XX such as cancer, viral and bacterial infection or genetic, primary or
XX combined immunodeficiency conditions including neutropenia or HIV
XX infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX in a biological sample in vitro or in vivo, as well as during gene
XX therapy procedures. The current sequence is that of the human anti-CD40
XX antibody variable region heavy chain protein of the invention.
XX
XX Sequence 471 AA;
XX
XX Query Match 73.7%; Score 580.5; DB 7; Length 471;
XX Best Local Similarity 72.4%; Pred. No. 3.2e-42;
XX Matches 113; Conservative 11; Mismatches 23; Indels 9; Gaps 1;
XX
XX QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVGYTLTSLPVMHWQAP 60
XX Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVGYTLTSLPVMHWQAP 60
XX
XX QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP 120
XX Db 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVP 120
XX
XX QY 121 -----DAFDIWGGQGTMTVSSASTKGPSVFPPL 147
XX Db 121 LGYCTNGVCSYFDYWGQGTMTVSSASTKGPSVFPPL 156
XX
XX RESULT 9
XX AAB36210
XX ID AAB36210 standard; protein; 467 AA.
XX
XX AC AAB36210;
XX
XX DT 15-FEB-2001 (first entry)
XX
XX DE Human immune system associated protein HISAP-8.
XX
XX Human; immune system associated protein; HISAP-8; immune disorder;
XX infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
XX OS US6135941-A.
XX PN
```

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XX PD 24-OCT-2000.
XX PF 27-MAR-1998; 98US-00049672.
XX PR 27-MAR-1998; 98US-00049672.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Tang YT, Yue H, Lam P, Corley NC, Guegler KJ, Baughn MR;
XX PI Hillman JL, Au-Yang J;
XX DR WPI: 2001-030926/04.
XX DR N-PSDB; AAC66526.
XX PT New human immune system associated proteins (HISAP) and polynucleotides
XX PT encoding the HISAP, useful for diagnosing, treating or preventing immune
XX PT or cell proliferative disorders or infections.
XX PS Claim 1; Col 61-64; 54pp; English.
XX PS The present invention provides the coding and protein sequences for a
XX CC number of human immune system associated proteins (HISAPs). These can be
XX CC used in the diagnosis and treatment of various autoimmune disorders,
XX CC infections and cell proliferation diseases. The diseases include AIDS,
XX CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
XX CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
XX CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
XX CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX SQ Sequence 467 AA;
Query Match 71.5%; Score 563.5; DB 4; Length 467;
Best Local Similarity 73.0%; Pred. No. 9.5e-41;
Matches 108; Conservative 19; Mismatches 20; Indels 1; Gaps 1;
QY 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWVQAP 60
DB 1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVQVSGTSLDLSVHWVQAP 60
QY 61 GKGLEWVGSPDPESGESIYAREFGSVTMTADTSDIAYMELSLRSDDTAVYCAVPDP 120
DB 61 GQGLEWNGGLAPENGEAVYAKFLGRLTSLSDTSADTAYMFLNLSGSDSAIYYCARQHY 120
QY 121 D-AFDINGQGTMTVTVSSASTKGPSVFPL 147
DB 121 DFFDFEWGQGTMTVTVSSASTKGPSVFPL 148
RESULT 10
AAI96302
ID AAY96302 standard; protein; 219 AA.
XX AC AAY96302;
XX DT 16-AUG-2000 (first entry)
XX DE Human IGFAM-14 immunoglobulin.
XX KW Human; immunoglobulin; IGFAM-14; IGFAM; immune disorder; cancer;
XX KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..119
XX FT Protein 20..219 /label= signal_peptide
XX FT Protein 34..117 /label= IGFAM-14
XX FT Domain /label= Ig_domain
XX OS WO2000029583-A2.

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XX PD 25-MAY-2000.
XX PF 19-NOV-1999; 99WO-US027566.
XX PR 19-NOV-1998; 98US-00195853.
XX PR 22-DEC-1998; 98US-0113635P.
XX PR 07-APR-1999; 99US-0128194P.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX PI Lu DAM, Lal P, Hillman JL, Yang J;
XX DR WPI: 2000-387796/33.
XX DR N-PSDB; AAA27394.
XX PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX PT protein is useful for preventing and treating disorders associated with
XX PT altered levels of the protein such as cancer, immune system disorders.
XX PS Claim 1; Page 88-89; 105pp; English.
XX PS The present sequence is the human immunoglobulin superfamily protein
XX CC IGFAM-14. Its Gene was isolated from a cDNA library of gallbladder
XX CC tissue. It is expressed in reproductive, gastrointestinal and
XX CC cardiovascular tissue, where cancer and inflammation are common. The
XX CC gene, protein, its antibodies, agonists and antagonists are suitable for
XX CC diagnosing and treating many diseases, including cancer, immune system
XX CC disorders (such as inflammation, AIDS, allergies, anaemia,
XX CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX CC systemic lupus erythematosus and ulcerative colitis), complications of
XX CC cancer, haemodialysis and extracorporeal circulation, trauma and
XX CC haematopoietic cancer (such as leukaemia) and infections caused by
XX CC bacteria, viruses, fungi or parasites
XX SQ Sequence 219 AA;
Query Match 69.2%; Score 545.5; DB 3; Length 219;
Best Local Similarity 69.7%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 5; Gaps 1;
QY 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWVQAP 60
DB 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWVQAP 60
QY 61 GKGLEWVGSPDPESGESIYAREFGSVTMTADTSDIAYMELSLRSDDTAVYCA--- 116
DB 61 GQGLEWNGWNTNPNSGGARYAQGFGLVTMTDTSISTAYLELRSLRSDGSAVYFCARQTT 120
QY 117 -VPDPAFDINGQGTMTVTVSSASTKGPSVFPL 147
DB 121 SSPVGDAFDINGQGTMTVTVSSASTKGPSVFPL 152
RESULT 11
AAW88464
ID AAW88464 standard; protein; 476 AA.
XX AC AAW88464;
XX DT 10-MAY-1999 (first entry)
XX DE Monoclonal antibody 4B5 heavy chain variable region.
XX KW Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
XX KW diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
XX KW lung carcinoma; metastasis; anti-idiotypic antibody; GD2 antigen; human.
XX OS Homo sapiens.
XX

```

```

PN WO9902545-A2.
XX
XX 21-JAN-1999.
XX
XX 08-JUL-1998; 98WO-IE001046.
XX
XX 08-JUL-1997; 97US-0051945P.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Dan MD;
XX
XX WPI; 1999-120769/10.
XX
XX N-PSDB; AAX06951.
XX
XX New antibody 4B5 polynucleotides and polypeptides - used to develop
XX products for the diagnosis and treatment of cancers and for prophylactic
XX therapy to reduce risk of recurrence.
XX
XX Claim 1; Page 79-80; 83pp; English.
XX
XX This polypeptide comprises the heavy chain variable region of the
XX recombinant human monoclonal antibody (Mab) 4B5. 4B5 recognises
XX antibodies specific for GD2 antigen antibodies. Antibodies specific for
XX GD2 recognise various cancers including glioblastoma, neuroblastoma,
XX malignant and/or metastatic melanoma, breast adenocarcinoma, lung
XX adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
XX prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
XX immunologic specificity for antibodies specific for GD2. These
XX derivatives, or antigen binding fragments, comprise regions of the 4B5
XX VDJ function and regions spanning the 4B5 CDRs. Other derivatives include
XX Fab, F(ab')2, Fab', scfv and isolated heavy and light chains (see also
XX AAW8465). Polynucleotide fragments (see AAX06951-54) encoding 4B5
XX antibody V regions are also provided, and therapeutic plasmids and
XX vectors, including vaccinia virus vectors, comprising these
XX polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
XX useful in generating a host immune response to cancer. Products of the
XX invention can be used in the detection and treatment of e.g. astrocytoma,
XX oligodendroglioma, ependymoma, medulloblastoma, primitive neural
XX ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
XX large cell lung adenocarcinomas, squamous cell carcinoma,
XX bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
XX hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
XX adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
XX uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
XX transitional squamous cell carcinoma of the bladder, B and T cell
XX lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
XX malignant melanoma, soft tissue sarcoma and leiomyosarcoma
XX
XX Sequence 476 AA;
XX
XX Query Match 68.4%; Score 539; DB 2; Length 476;
XX Best Local Similarity 66.9%; Pred. No. 1.3e-38;
XX Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;
XX
XX 1 MDWTWRLFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
XX
XX 1 MDWTWRLFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
XX
XX 61 GKGLEWVGSFDPGSGESIIYAREFOGSVTMTADTSTDIAYMELSLRSDDTAVYVC 115
XX
XX 61 GQGLEWVGMWNPNSGKTGYAQKTQGRVTYTRNTSIRTAYMELSLGRLSDTAVYFCARNAD 120
XX
XX 116 ----AVPDPAEDFINGGGTWTVTSSASTKGPSPVFL 147
XX
XX 121 NVENAAIYHYGMDVWGQGTITVTSSASTKGPSPVFL 157
XX
XX
XX RESULT 12
XX AAW48650
XX AAW48650 standard; protein; 652 AA.
XX
XX AAW48650;
XX

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XX 04-AUG-1998 (first entry)
XX
XX Heavy chain of hmb425 fused to TNF alpha.
XX
XX Antibody-cytokine fusion protein; tricitronic vector; chimeric;
XX TNF alpha; IL-2; IRES; internal ribosome entry site.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1.494
XX /note= "Heavy chain of human mAb 425"
XX Region 495..652
XX /note= "TNF alpha"
XX
XX WO9811241-A1.
XX
XX 19-MAR-1998.
XX
XX 02-SEP-1997; 97WO-EP004765.
XX
XX 16-SEP-1996; 96EP-00114820.
XX 30-SEP-1996; 96EP-00115635.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E, Weige T;
XX Hauser H, Mielke C;
XX
XX WPI; 1998-207400/18.
XX N-PSDB; AAV18096.
XX
XX Oligocitronic expression vector - useful for production of, e.g.
XX MAb425/TNF- $\alpha$  or MAb425/IL-2 antibody fusion protein.
XX
XX Disclosure; Fig 15; 89pp; English.
XX
XX The present sequence represents a fusion protein comprising of TNF alpha
XX fused to the C-terminus of the heavy chain of the human monoclonal
XX antibody 425 (hmb425). The hmb425 has specificity for the human EGF
XX receptor. The invention claims for a new pMCDHAP tricitronic vector
XX (AAV18096) for the expression of an antibody-cytokine fusion protein,
XX hmb425-TNF alpha. The TNF alpha sequence can be substituted by the IL-2
XX sequence. The vector also contains a strong promoter/enhancer unit, a
XX selection marker gene and at least two poliovirus derived internal
XX ribosomal entry site (IRES) sequences. The vector can be expressed in
XX mammalian host cells for the production of heteromeric fusion proteins.
XX This expression system is claimed to produce the heteromeric proteins in
XX high yields
XX
XX Sequence 652 AA;
XX
XX Query Match 68.0%; Score 536; DB 2; Length 652;
XX Best Local Similarity 60.6%; Pred. No. 3.4e-38;
XX Matches 106; Conservative 14; Mismatches 27; Indels 28; Gaps 2;
XX
XX 1 MDWTWRLFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
XX
XX 1 MDWTWRLFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
XX
XX 61 GKGLEWVGSFDPGSGESIIYAREFOGSVTMTADTSTDIAYMELSLRSDDTAVYVC 120
XX
XX 61 GQGLEWIGEFNPNNGRTNYNEKPKSKATMTVDTSTNTAYMELSLRSDDTAVYVCASRDY 120
XX
XX 121 D----AFDIWGGTWTVTSS-----ASTKGPSPVFL 147
XX
XX 121 DYDGRYFDYWGQGTITVTSSGENILCAWAQLCTPFRSHGTTSLAASKGPSPVFL 175
XX
XX
XX RESULT 13
XX AAR77610
XX

```


AA777610 standard; protein; 249 AA.

AA777610;

25-MAR-2003 (revised)

15-MAR-1996 (first entry)

XX

Humanised 5G1.1 VH + IGHL.

DE

XX

Complement C5; haemolysis; kidney; glomerulonephritis;

KW

monoclonal antibody; antiinflammatory; antibody engineering;

KW

humanised antibody; complementarity determining region; CDR.

KW

XX

Synthetic.

OS

XX

Key Location/Qualifiers

XX

Peptide 1..19

FT

/label= sig_peptide

FT

Peptide 20..249

FT

/label= mat_peptide

FT

Region 45..54

FT

/label= CDR-H1

FT

Region 65..79

FT

/label= CDR-H2

FT

Region 118..130

FT

/label= CDR-H3

FT

WO9529697-A1.

XX

09-NOV-1995.

XX

01-MAY-1995; 95WO-US005689.

XX

02-MAY-1994; 94US-00236208.

XX

(ALEX-) ALEXION PHARM INC.

PA

Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;

PI

Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;

PI

WPI; 1995-392923/50.

XX

N-PSDB; AATC8483.

DR

Treating glomerulonephritis with antibody against complement C5 component

PT

- to inhibit complement induced cell lysis.

PT

Example 11; Page 119-122; 181pp; English.

XX

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +

CC

IGHL (AA777610), includes CDRs derived from mouse anti-C5 monoclonal

CC

antibody 5G1.1. It can be co-expressed with a humanised light chain

CC

(AA777612) in human 293 EBNA cells using encoding DNAs subcloned into

CC

vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain

CC

the ability of Mab 5G1.1 to block human complement C5a generation and

CC

thus to reduce glomerular inflammation and kidney dysfunction associated

CC

with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)

CC

XX

SQ

Sequence 249 AA;

Query Match 68.0%; Score 535.5; DB 2; Length 249;

Best Local Similarity 69.1%; Pred. No. 1.3e-38;

Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 MDWTWELLFLVAAAGTAAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWVQAP 60

DB 1 MKNSWVILFLVLTAGVSHQVQLVQSGAEVKKPGASVKVSCKAGYIFSNYIOWVQAP 60

QY 61 GKGLWVSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116

DB 61 GQGLEWGMGILFGSGSTEVYAKFQGRVTMTADTSTDIAYMELSLRSDDTAVYYCARYFF 120

QY 117 VDPDP-APDINGCGTNTVSSASTKGPSVFPL 147

AA777610 standard; protein; 249 AA.

AA777610;

25-MAR-2003 (revised)

15-MAR-1996 (first entry)

XX

Humanised 5G1.1 VH + IGHL.

DE

XX

Complement C5; haemolysis; kidney; glomerulonephritis;

KW

monoclonal antibody; antiinflammatory; antibody engineering;

KW

humanised antibody; complementarity determining region; CDR.

KW

XX

Synthetic.

OS

XX

Key Location/Qualifiers

XX

Peptide 1..19

FT

/label= sig_peptide

FT

Peptide 20..249

FT

/label= mat_peptide

FT

Region 45..54

FT

/label= CDR-H1

FT

Region 65..79

FT

/label= CDR-H2

FT

Region 118..130

FT

/label= CDR-H3

FT

WO9529697-A1.

XX

09-NOV-1995.

XX

01-MAY-1995; 95WO-US005689.

XX

02-MAY-1994; 94US-00236208.

XX

(ALEX-) ALEXION PHARM INC.

PA

Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;

PI

Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;

PI

WPI; 1995-392923/50.

XX

N-PSDB; AATC8483.

DR

Treating glomerulonephritis with antibody against complement C5 component

PT

- to inhibit complement induced cell lysis.

PT

Example 11; Page 119-122; 181pp; English.

XX

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +

CC

IGHL (AA777610), includes CDRs derived from mouse anti-C5 monoclonal

CC

antibody 5G1.1. It can be co-expressed with a humanised light chain

CC

(AA777612) in human 293 EBNA cells using encoding DNAs subcloned into

CC

vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain

CC

the ability of Mab 5G1.1 to block human complement C5a generation and

CC

thus to reduce glomerular inflammation and kidney dysfunction associated

CC

with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)

CC

XX

SQ

Sequence 249 AA;

Query Match 68.0%; Score 535.5; DB 2; Length 249;

Best Local Similarity 69.1%; Pred. No. 1.3e-38;

Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 MDWTWELLFLVAAAGTAAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWVQAP 60

DB 1 MKNSWVILFLVLTAGVSHQVQLVQSGAEVKKPGASVKVSCKAGYIFSNYIOWVQAP 60

QY 61 GKGLWVSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116

DB 61 GQGLEWGMGILFGSGSTEVYAKFQGRVTMTADTSTDIAYMELSLRSDDTAVYYCARYFF 120

QY 117 VDPDP-APDINGCGTNTVSSASTKGPSVFPL 147

AA777610 standard; protein; 249 AA.

AA777610;

25-MAR-2003 (revised)

15-MAR-1996 (first entry)

XX

Humanised 5G1.1 VH + IGHL.

DE

XX

Complement C5; haemolysis; kidney; glomerulonephritis;

KW

monoclonal antibody; antiinflammatory; antibody engineering;

KW

humanised antibody; complementarity determining region; CDR.

KW

XX

Synthetic.

OS

XX

Key Location/Qualifiers

XX

Peptide 1..19

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/label= sig_peptide

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Peptide 20..249

FT

/label= mat_peptide

FT

Region 45..54

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/label= CDR-H1

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Region 65..79

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/label= CDR-H2

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Region 118..130

FT

/label= CDR-H3

FT

WO9529697-A1.

XX

09-NOV-1995.

XX

01-MAY-1995; 95WO-US005689.

XX

02-MAY-1994; 94US-00236208.

XX

(ALEX-) ALEXION PHARM INC.

PA

Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;

PI

Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;

PI

WPI; 1995-392923/50.

XX

N-PSDB; AATC8483.

DR

Treating glomerulonephritis with antibody against complement C5 component

PT

- to inhibit complement induced cell lysis.

PT

Example 11; Page 119-122; 181pp; English.

XX

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +

CC

IGHL (AA777610), includes CDRs derived from mouse anti-C5 monoclonal

CC

antibody 5G1.1. It can be co-expressed with a humanised light chain

CC

(AA777612) in human 293 EBNA cells using encoding DNAs subcloned into

CC

vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain

CC

the ability of Mab 5G1.1 to block human complement C5a generation and

CC

thus to reduce glomerular inflammation and kidney dysfunction associated

CC

with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)

CC

XX

SQ

Sequence 249 AA;

Query Match 68.0%; Score 535.5; DB 2; Length 249;

Best Local Similarity 69.1%; Pred. No. 1.3e-38;

Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 MDWTWELLFLVAAAGTAAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWVQAP 60

DB 1 MKNSWVILFLVLTAGVSHQVQLVQSGAEVKKPGASVKVSCKAGYIFSNYIOWVQAP 60

QY 61 GKGLWVSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116

DB 61 GQGLEWMGILFGSGSTEVYAKFQGRVTMTADTSTDIAYMELSLRSDDTAVYYCAR YFF 120

QY 117 VDPDP-APDINGCGTMTVSSASTKGPSVFPL 147

AA777610 standard; protein; 249 AA.

AA777610;

25-MAR-2003 (revised)

15-MAR-1996 (first entry)

XX

Humanised 5G1.1 VH + IGHL.

DE

XX

Complement C5; haemolysis; kidney; glomerulonephritis;

KW

monoclonal antibody; antiinflammatory; antibody engineering;

KW

humanised antibody; complementarity determining region; CDR.

KW

XX

Synthetic.

OS

XX

Key Location/Qualifiers

XX

Peptide 1..19

FT

/label= sig_peptide

FT

Peptide 20..249

FT

/label= mat_peptide

FT

Region 45..54

FT

/label= CDR-H1

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Region 65..79

FT

/label= CDR-H2

FT

Region 118..130

FT

/label= CDR-H3

FT

WO9529697-A1.

XX

09-NOV-1995.

XX

01-MAY-1995; 95WO-US005689.

XX

02-MAY-1994; 94US-00236208.

XX

(ALEX-) ALEXION PHARM INC.

PA

Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;

PI

Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;

PI

WPI; 1995-392923/50.

XX

N-PSDB; AATC8483.

DR

Treating glomerulonephritis with antibody against complement C5 component

PT

- to inhibit complement induced cell lysis.

PT

Example 11; Page 119-122; 181pp; English.

XX

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +

CC

IGHL (AA777610), includes CDRs derived from mouse anti-C5 monoclonal

CC

antibody 5G1.1. It can be co-expressed with a humanised light chain

CC

(AA777612) in human 293 EBNA cells using encoding DNAs subcloned into

CC

vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain

CC

the ability of Mab 5G1.1 to block human complement C5a generation and

CC

thus to reduce glomerular inflammation and kidney dysfunction associated

CC

with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)

CC

XX

SQ

Sequence 249 AA;

Query Match 68.0%; Score 535.5; DB 2; Length 249;

Best Local Similarity 69.1%; Pred. No. 1.3e-38;

Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 MDWTWELLFLVAAAGTAAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWVQAP 60

DB 1 MKNSWVILFLVLTAGVSHQVQLVQSGAEVKKPGASVKVSCKAGYIFSNYIOWVQAP 60

QY 61 GKGLWVSGFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116

DB 61 GQGLEWMGILFGSGSTEVYAKFQGRVTMTADTSTDIAYMELSLRSDDTAVYYCAR YFF 120

QY 117 VDPDP-APDINGCGTMTVSSASTKGPSVFPL 147

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XX AC ABU08022;
XX DT 10-MAY-2003 (first entry)
XX DE Monoclonal rabies virus antibody heavy chain, clone 57.
XX KW Human; antibody; constant region; monoclonal antibody 57; Mab 57;
XX KW variable region; Rabies; neurological disease; infection;
XX KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
XX KW pathogen; vaccine; virucide; heavy chain.
XX OS Homo sapiens.
XX PN WO2003016501-A2.
XX PD 27-FEB-2003.
XX PF 21-AUG-2002; 2002WO-US026584.
XX PR 21-AUG-2001; 2001US-0314023P.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Hooper DC, Dietzschold B;
XX DR WPI; 2003-278566/27.
XX DR N-PSDB; ABX12864.
XX PT New recombinant antibody comprising a constant region of Mab 57 linked to
XX PT a non-Mab 57 variable region, useful for treating an individual exposed
XX PT to a pathogen, e.g. rabies infection.
XX PS Claim 1; Page 38; 38pp; English.
XX CC The invention discloses a recombinant antibody comprising a constant
XX CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
XX CC region. Rabies is an acute, neurological disease caused by infection of
XX CC the central nervous system with the rabies virus, a member of the
XX CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
XX CC for producing an isolated recombinant antibody by culturing a host cell,
XX CC containing a recombinant expression vector comprising the nucleic acid
XX CC molecule encoding the antibody, and isolating the recombinant antibody
XX CC expressed and treating an individual exposed to a pathogen by
XX CC administering to the individual the recombinant antibody. The recombinant
XX CC antibodies are useful for preventing (vaccine) and treating an individual
XX CC exposed to a pathogen, e.g. rabies infection. They are also useful for
XX CC the qualitative and quantitative determination of the rabies virus. The
XX CC sequences presented are the antibody protein fragments, the nucleic acids
XX CC encoding them or the PCR primers used to construct the recombinant
XX CC expression vector
XX SQ Sequence 476 AA;

Query Match 67.5%; Score 532; DB 6; Length 476;
Best Local Similarity 67.5%; Pred. NO. 5.3e-38;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDKWTIRILFLVAATGTHAQVLQSGAEVKPGASVKVCKVSGVTLTLPVHWGOAP 60
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QY 61 GKGLEWVGSFDPESGESIYAREFQGSVMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
DQ 61 GKGLEWVGGIIPFGTANYAQRFGRLTITADESTAYMELSLRSDDTAVYYFCARENL 120
QY 121 DA-----FDIWGGTMTVSSASTKGPSVPL 147
DQ 121 DNSGTYYFSGWFDPPWGGTTLTVSSASTKGPSVPL 157

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Search completed: April 5, 2004, 13:24:15
Job time : 50.4772 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 35.2792 Seconds
(without alignments)
1116.513 Million cell updates/sec

Title: US-10-044-569B-2

Perfect score: 788
Sequence: 1 MDWTWRIILFLVAAATGTHAQ.....MTVSSASTKGPSVFPLGSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788	100.0	150	14	US-10-044-569B-2
2	627.5	79.6	146	14	US-10-390-986-12
3	625.5	79.4	146	14	US-10-390-986-10
4	590	74.9	470	9	US-09-859-053-28
5	539	68.4	476	9	US-09-747-669-3
6	539	68.4	476	14	US-10-290-703-3
7	532	67.5	476	14	US-10-225-108A-16
8	532	67.5	476	15	US-10-461-148-9
9	525	66.6	470	14	US-10-216-484-143
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11	525	66.6	470	14	US-10-384-933-143
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15	523	66.4	470	14	US-10-216-484-157

16	523	66.4	470	14	US-10-384-933-157
17	522	66.2	470	14	US-10-216-484-117
18	522	66.2	470	14	US-10-384-933-117
19	521.5	66.2	197	15	US-10-264-049-4263
20	518.5	65.8	515	9	US-09-825-012-66
21	518.5	65.8	517	9	US-09-825-012-38
22	518.5	65.8	519	9	US-09-825-012-76
23	518.5	65.8	519	9	US-09-825-012-80
24	518.5	65.8	519	9	US-09-825-012-71
25	518.5	65.8	521	9	US-09-825-012-61
26	518.5	65.8	525	9	US-09-825-012-85
27	518.5	65.8	527	9	US-09-825-012-43
28	518.5	65.8	529	9	US-09-825-012-95
29	518.5	65.8	531	9	US-09-825-012-90
30	518.5	65.8	729	9	US-09-825-012-52
31	518.5	65.8	730	9	US-09-825-012-49
32	518.5	65.8	731	9	US-09-825-012-46
33	518.5	65.8	739	9	US-09-825-012-61
34	518.5	65.8	740	9	US-09-825-012-58
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36	516	65.5	574	13	US-10-047-542-45
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ALIGNMENTS

RESULT 1

US-10-044-569B-2
; Sequence 2, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (130)..(159)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202)..(258)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (343)..(375)
; OTHER INFORMATION: complementary determining region number three
; US-10-044-569B-2

Query Match 100.0%; Score 788; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 4, 5e-63;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDWTWRIILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPWHVWGQAP 60
Db 1 MDWTWRIILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPWHVWGQAP 60
QY 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
Db 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
QY 121 DAFDIWGQGTMTVTVSSASTKGPSVFPLGSR 150
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RESULT 2
US-10-390-986-12
; Sequence 12, Application US/10390986
; Publication No. US20030166011A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-12

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Best Local Similarity 84.2%; Pred. No. 1.1e-48;
Matches 123; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

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Db 1 MDCTWRIILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAP 60
QY 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 117
Db 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCATSTV 120

RESULT 3
US-10-390-986-10
; Sequence 10, Application US/10390986
; Publication No. US20030166011A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
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; NUMBER OF SEQ ID NOS: 27
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; SEQ ID NO 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-10

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Db 1 MDCTWRIILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAP 60
QY 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 117
Db 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCATSTV 120

RESULT 4
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

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Matches 117; Conservative 8; Mismatches 22; Indels 8; Gaps 1;

QY 1 MDWTWRIILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPWHVWGQAP 60
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QY 61 KGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 118
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RESULT 5
US-09-747-669-3
; Sequence 3, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-3

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Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

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; Publication No. US20030118593A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match      68.4%; Score 539; DB 14; Length 476;
Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

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DB 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
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DB 61 GQGLEWGMWNPNSGKTGYAQKFGQVTRTNTSIRTAYMELSLRSEDVAVYFCARNAD 120
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157

RESULT 7
US-10-225-108A-16
; Sequence 16, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

Query Match      67.5%; Score 532; DB 14; Length 476;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFQGSVVTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
DB 61 GQGLEWGMWGGIIPFGTANYAQRFGRLTITADESTSTAYMELSSLRSDDTAVYFCARENL 120
QY 121 DA-----FDINGQGTMTVSSASTKGPSVFPL 147
DB 121 DNSGTYFFSGWFDPMWGQGTITVSSASTKGPSVFPL 157

RESULT 8
US-10-461-148-9
; Sequence 9, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; APPLICANT: Hooper, Douglas C.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
```

```
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-3

Query Match      68.4%; Score 539; DB 9; Length 476;
Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFQGSVVTADTSTDIAYMELSSLRSDDTAVYYC----- 115
DB 61 GKGLWVGSFDPESGESIYAREFQGSVVTADTSTDIAYMELSSLRSDDTAVYYC----- 115
QY 61 GQGLEWGMWNPNSGKTGYAQKFGQVTRTNTSIRTAYMELSLRSEDVAVYFCARNAD 120
DB 61 GQGLEWGMWNPNSGKTGYAQKFGQVTRTNTSIRTAYMELSLRSEDVAVYFCARNAD 120
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157

RESULT 7
US-10-225-108A-16
; Sequence 16, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

Query Match      67.5%; Score 532; DB 14; Length 476;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFQGSVVTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
DB 61 GQGLEWGMWGGIIPFGTANYAQRFGRLTITADESTSTAYMELSSLRSDDTAVYFCARENL 120
QY 121 DA-----FDINGQGTMTVSSASTKGPSVFPL 147
DB 121 DNSGTYFFSGWFDPMWGQGTITVSSASTKGPSVFPL 157

RESULT 8
US-10-461-148-9
; Sequence 9, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; APPLICANT: Hooper, Douglas C.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
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Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDISTAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFINGQGTMTVSSASTKGPSVPEL 147
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVPEL 151

RESULT 12
US-10-384-933-147
; Sequence 147, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-147

Query Match 66.6%; Score 525; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDISTAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFINGQGTMTVSSASTKGPSVPEL 147
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVPEL 151

RESULT 13
US-10-216-484-145
; Sequence 145, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG

CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 145
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-145

Query Match 66.5%; Score 524; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 7.8e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDISTAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFINGQGTMTVSSASTKGPSVPEL 147
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVPEL 151

RESULT 14
US-10-384-933-145
; Sequence 145, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 145
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-145

Query Match 66.5%; Score 524; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 7.8e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDISTAYMELSLRSDDTAVYYCARNRD 120

QY 117 VPDPAFDIWGGTMTVTVSSASTKGPSVFPL 147
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPL 151

RESULT 15

US-10-216-484-157
; Sequence 157, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Takashi, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157

Query Match 66.4%; Score 523; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 9.6e-39;
Matches 103; Conservative 15; Mismatches 29; Indels 4; Gaps 1;
QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWYQAP 60
Db 1 MGNSCIILFLVATATGTHSQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWYQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCA--- 116
Db 61 QQGLEWGEIDPSPSYNYNQKFKGRVTITRTDTSTAYMELSLRSEDVAVYYCARNRD 120
QY 117 VPDPAFDIWGGTMTVTVSSASTKGPSVFPL 147
Db 121 YSNWYFDVWGEGTLTVTVSSASTKGPSVFPL 151

Search completed: April 5, 2004, 13:59:12
Job time : 36.2792 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:36:42 ; Search time 13.4518 Seconds
(without alignments)
575.678 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTWRILFLVAAATGTHAQ.....MTVSSASTKGPSVPLGSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	627.5	79.6	146	4	US-09-582-337-12
2	625.5	79.4	146	4	US-09-582-337-10
3	583.5	71.5	467	3	US-09-049-672A-8
4	535	67.9	117	3	US-08-545-809A-110
5	522.5	66.3	236	3	US-09-049-672A-13
6	513.5	65.2	137	3	US-08-513-968-38
7	512.5	65.0	467	2	US-07-916-098A-45
8	504	64.0	476	2	US-08-378-939-10
9	503	63.8	472	4	US-09-301-593-43
10	501	63.6	140	1	US-07-946-421-28
11	496	62.9	149	4	US-09-582-337-8
12	492.5	62.5	135	1	US-08-137-117D-102
13	492.5	62.5	135	2	US-08-436-717-102
14	492	62.4	136	3	US-08-649-100-41
15	488.5	62.0	135	1	US-08-137-117D-100
16	488.5	62.0	135	2	US-08-436-717-100
17	486	61.7	138	3	US-08-513-968-44
18	485.5	61.6	139	4	US-09-355-925-7
19	482.5	61.2	133	3	US-08-718-323A-8
20	482.5	61.2	133	4	US-09-587-526-8
21	481.5	61.1	139	4	US-09-355-925-8
22	479.5	60.9	135	1	US-08-137-117D-112
23	479.5	60.9	135	2	US-08-436-717-112
24	474	60.2	136	3	US-08-648-265A-99
25	472	59.9	117	3	US-08-545-809A-90
26	470.5	59.7	147	1	US-08-217-918-4
27	470	59.6	142	2	US-08-561-521-17

28	470	59.6	142	5	PCT-US95-01219-17	Sequence 17, Appl
29	463.5	58.8	135	1	US-07-634-278-19	Sequence 19, Appl
30	463.5	58.8	135	1	US-08-477-728-19	Sequence 19, Appl
31	463.5	58.8	135	1	US-08-474-040-19	Sequence 19, Appl
32	463.5	58.8	135	1	US-08-487-200-19	Sequence 19, Appl
33	463.5	58.8	135	2	US-08-303-569B-31	Sequence 31, Appl
34	463.5	58.8	135	3	US-08-484-337-19	Sequence 19, Appl
35	463	58.8	140	3	US-08-579-378A-12	Sequence 12, Appl
36	463	58.8	140	5	PCT-US93-11612-12	Sequence 12, Appl
37	462.5	58.7	139	1	US-08-253-877C-19	Sequence 19, Appl
38	462.5	58.7	139	2	US-08-452-164A-19	Sequence 18, Appl
39	462.5	58.7	139	3	US-08-603-024-18	Sequence 18, Appl
40	462.5	58.7	139	4	US-08-450-809-14	Sequence 14, Appl
41	462	58.6	142	2	US-08-476-768-14	Sequence 14, Appl
42	462	58.6	142	3	US-08-127-721A-14	Sequence 14, Appl
43	462	58.6	142	3	US-08-485-246A-14	Sequence 14, Appl
44	460	58.4	140	3	US-08-836-561-63	Sequence 63, Appl
45	460	58.4	140	4	US-09-434-122-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-582-337-12
; Sequence 12, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582.337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-12

Query Match	79.6%	Score 627.5;	DB 4;	Length 146;
Best Local Similarity	84.2%	Pred. No. 4.2e-51;		
Matches 123;	Conservative	7;	Mismatches 13;	Indels 3; Gaps 1;
QY	1	MDWTWRILFLVAAATGTHAQVQLVQSGAEVKVSKVSKVSGYTLTLPVHWVQAP	60	
Db	1	MDCTWRIFLVAATGTHAQVQLVQSGAEVKVSKVSKVSGYTLTLPVHWVQAP	60	
QY	61	GKGLEWGSFPDSEGESIYAREFGSVTWTADTDTDAYMELSLRSDDTAVYYCA--V	117	
Db	61	GKGLEWGSFPDSEGESIYAREFGSVTWTADTDTDAYMELSLRSDDTAVYYCA--V	120	
QY	118	PDPADFHWGQGTMTVSSASTKGPS	143	
Db	121	VTPWFYDWGQGTMTVSSASTKGPS	146	

RESULT 2
US-09-582-337-10
; Sequence 10, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582.337

;; CURRENT FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: JP P1997-367699
;; PRIOR FILING DATE: 1997-12-25
;; PRIOR APPLICATION NUMBER: JP P1998-356183
;; PRIOR FILING DATE: 1998-12-15
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 10
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-582-337-10

Query Match 79.4%; Score 625.5; DB 4; Length 146;
Best Local Similarity 84.2%; Pred. No. 6.4e-51;
Matches 123; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWYGOAP 60
DB 1 MDCWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWYGOAP 60

QY 61 GKGLEWVSGFPDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---V 117
DB 61 GKGLEWVSGFPDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCATSTV 120

QY 118 PDPADPWGQGTWTVSSASTKGPS 143
DB 121 VTPWYFDYWGQGTLLTVSSASTKGPS 146

RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Mariah R.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 467 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: LUNGPUT11
;; CLONE: 2747531
US-09-049-672A-8

Query Match 71.5%; Score 563.5; DB 3; Length 467;
Best Local Similarity 73.0%; Pred. No. 1.4e-44;
Matches 108; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWYGOAP 60
DB 1 MDCWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWYGOAP 60

QY 61 GKGLEWVSGFPDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDF 120
DB 61 GCGLEWVSGFPDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDF 120

QY 121 D-AFDWQGTWTVSSASTKGPSVFPL 147
DB 121 DFFDFWQGTWTVSSASTKGPSVFPL 148

RESULT 4
US-08-545-809A-110
; Sequence 110, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-110

Query Match 67.9%; Score 535; DB 3; Length 117;
Best Local Similarity 87.9%; Pred. No. 1.3e-42;

```
Matches 102; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWGQAP 60
DB 1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAP 60
QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
DB 61 GKGLWVGSGFDPEDGETIYIAQKPGQVMTEDTSTDIAYMELSLRSDDTAVYYCA 116

RESULT 5
US-09-049-672A-13
; Sequence 13, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Marian R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNNOT01
; CLONE: 3551457
US-09-049-672A-13

Query Match 66.3%; Score 522.5; DB 3; Length 236;
Best Local Similarity 67.3%; Pred. No. 4e-41;
Matches 101; Conservative 16; Mismatches 30; Indels 3; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAP 60
QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA ---V 117
```

```
Db 61 GQLEWMGWINAGNGTKYSONFGQRTITRDTASATAYMELSLRSDDTAVYYCARVWA 120
QY 118 PDPAEDFMCGQTMVTVSSASTKGPSVFPL 147
Db 121 GEFTSFQYWGQGLTVTVSSASPTSPKVFRL 150

RESULT 6
US-08-513-968-38
; Sequence 38, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-968-38

Query Match 65.2%; Score 513.5; DB 3; Length 137;
Best Local Similarity 69.3%; Pred. No. 1.5e-40;
Matches 95; Conservative 16; Mismatches 25; Indels 1; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTLPVHWGQAP 60
DB 1 MDWTRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVCKASGTFITYTHWVRQAP 60
QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVP-D 119
DB 61 GQGLEWIGGINPNNGTSYTKFKGKATMTVDTSNTAYMELSLRSDDTAVYYCATPY 120
QY 120 PDPAEDFMCGQTMVTVSS 136
DB 121 AYADISWGQGLTVTVSS 137
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; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U. S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-10

Query Match 64.0%; Score 504; DB 2; Length 476;
Best Local Similarity 62.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 16; Mismatches 28; Indels 16; Gaps 2;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSGYTLTLPVHWVQAP 60
Db 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSGYTLTLPVHWVQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GKGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
QY 121 DA-----FDIWGGTMTVSSASTKGPSVFPL 147
Db 118 DRYQANFDRARVGVFDPWGQGLTVTVSSASTKGPSVFPL 157

RESULT 9
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29

; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U. S. A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-45

Query Match 65.0%; Score 512.5; DB 2; Length 467;
Best Local Similarity 64.5%; Pred. No. 7.4e-40;
Matches 98; Conservative 17; Mismatches 32; Indels 5; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSGYTLTLPVHWVQAP 60
Db 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSGYTLTLPVHWVQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GKGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
QY 121 DA-----FDIWGGTMTVSSASTKGPSVFPL 147
Db 121 NYATGAWFAYMGQGLTVTVSSASTKGPSVFPL 152

RESULT 8
US-08-378-939-10
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```
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo.sapiens
US-09-301-593-43

Query Match      63.8%; Score 503; DB 4; Length 472;
Best Local Similarity 63.8%; Pred. No. 5.7e-39;
Matches 98; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWGQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRFVCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKTSTYTTFTVTHVVRQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 GARLEWIGINPENGIPNTNQKGRATLVGKSASTAYMELSLRSEDTAVYYCARRRI 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 117 ---VPDPAFDIWGQGTWTVSSASTKGPSVFPL 147
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 AYCDEGHAMDYWGQGLTVTVSS-STKGPSVFPL 153
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
US-07-946-421-28
; Sequence 28, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettlesborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-28

Query Match      63.6%; Score 501; DB 1; Length 140;
Best Local Similarity 68.6%; Pred. No. 2.2e-39;
Matches 96; Conservative 14; Mismatches 26; Indels 4; Gaps 1;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWGQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRFVCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSSHMHVVRQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 GQGLEWVGEPNPNNGRINTYNEKFSRVMTLDTSTAYMELSLRSEDTAVYYCASRDY 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 121 D----AFDIWGQGTWTVSS 136
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 DYDGRVFDYWGQGLTVTVSS 140
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
US-09-582-337-8
; Sequence 8, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: JI-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-8

Query Match      62.9%; Score 496; DB 4; Length 149;
Best Local Similarity 66.9%; Pred. No. 6.9e-39;
Matches 103; Conservative 9; Mismatches 26; Indels 16; Gaps 3;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKV-----SGYTLTELPVH 54
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKAFWLHLSPGYM-----H 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 55 WVGQAQPGKLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYY 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 56 WVRQAQPGQLEWVGNPNSSGTHYAQMFGQGVTVTRDTSTISAYMELSLRSDDTAVYY 115
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 115 CAVDPDPA-----FDIWGQGTWTVTVSSASTKGPS 143
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 116 CAREGIAAAIYGMVWGQGLTVTVSSASTKGPS 149
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 12
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
```

NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 62.5%; Score 492.5; DB 1; Length 135;
Best Local Similarity 68.4%; Pred. No. 1.3e-38;
Matches 93; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTWRYFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKVSGYTSYTIHWVRQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYCAVDPDP 120
Db 61 GQGLEWIGYIDPFNGGTSYNGKFKGVTMTVDTSTNTAYMELSLRSDTAVYCA-RGG 119
QY 121 DAFDWGGTMTVYSS 136
Db 120 NRPAYWGGTILVTYSS 135

RESULT 13
US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-102

Query Match 62.5%; Score 492.5; DB 2; Length 135;
Best Local Similarity 68.4%; Pred. No. 1.3e-38;
Matches 93; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTWRYFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKVSGYTSYTIHWVRQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYCAVDPDP 120
Db 61 GQGLEWIGYIDPFNGGTSYNGKFKGVTMTVDTSTNTAYMELSLRSDTAVYCA-RGG 119
QY 121 DAFDWGGTMTVYSS 136
Db 120 NRPAYWGGTILVTYSS 135

RESULT 14
US-08-649-100-41
Sequence 41, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-PAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-649-100-41

Query Match 62.4%; Score 492; DB 3; Length 136;
Best Local Similarity 68.4%; Pred. No. 1.5e-38;
Matches 93; Conservative 13; Mismatches 30; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
QY 61 GKLEWVGSPDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYICAVPDP 120
Db 61 GKLEWVGSPDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYICAVPDP 120
QY 121 DAFDINGGGTMTVTVSS 136
Db 121 DAFDINGGGTMTVTVSS 136

RESULT 15

US-08-137-117D-100
Sequence 100, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 62.0%; Score 488.5; DB 1; Length 135;
Best Local Similarity 68.4%; Pred. No. 3.1e-38;
Matches 93; Conservative 15; Mismatches 27; Indels 1; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRVFCLLAVAPGAHSQVQVQSGAEVKKPGASVKVSCKVSGYTSYIIHWVQAP 60
QY 61 GKLEWVGSPDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYICAVPDP 120
Db 61 GKLEWVGSPDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYICAVPDP 120
QY 121 DAFDINGGGTMTVTVSS 136
Db 121 DAFDINGGGTMTVTVSS 136

Search completed: April 5, 2004, 13:44:08
Job time : 14.4518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 11.533 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569b-4

Perfect score: 733
Sequence: 1 METPAQLLFLLLLWLPDTTG.....TRLEIKGTVAAPSVFIIPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	85.9	129	2 S49532	anti-Sm antibody V
2	627	85.5	145	2 S20631	IG kappa chain - h
3	624	85.1	129	1 K3H0HA	IG kappa chain pre
4	614	83.8	129	1 K3H0HI	IG kappa chain var
5	614	83.8	129	2 S46369	IG light chain var
6	614	83.8	134	2 S38643	IG kappa chain v r
7	608.5	83.0	144	2 PL0106	IG kappa chain pre
8	608	82.9	128	2 S20636	IG kappa chain v r
9	596	81.3	121	2 S40327	IG kappa chain - h
10	594	81.0	130	2 S20637	IG kappa chain v r
11	591	80.6	129	2 A32274	IG kappa chain pre
12	576	78.6	124	2 S20633	IG kappa chain - h
13	574	78.3	116	2 B27594	IG kappa chain pre
14	567.5	77.4	131	2 S40346	IG kappa chain v-J
15	563.5	76.9	126	2 S40325	IG kappa chain - h
16	560.5	76.5	116	2 C27594	IG kappa chain pre
17	557.5	76.1	128	1 K3H041	IG kappa chain pre
18	553	75.4	130	2 S40360	IG kappa chain - h
19	549	74.9	127	2 S40380	IG kappa chain v-J
20	547	74.6	116	2 B25521	IG kappa chain pre
21	540.5	73.7	128	2 S40343	IG kappa chain v-J
22	537	73.3	129	2 S40363	IG kappa chain - h
23	534.5	72.9	128	2 S40379	IG kappa chain v-J
24	533	72.7	215	2 JE0242	IG kappa chain NIG
25	532.5	72.6	114	2 S46375	IG kappa chain v-J
26	531.5	72.5	128	2 A56701	IG kappa chain v r
27	530	72.3	215	2 A23746	IG kappa chain v-I
28	522.5	71.3	129	2 S29627	IG kappa chain v r
29	520	70.9	109	2 B30601	IG kappa chain v-I

30 520 70.9 109 2 H30601 IG kappa chain v-I
31 519.5 70.9 125 2 S40344 IG kappa chain v-J
32 518 70.7 108 2 C30608 IG kappa chain v-I
33 517 70.5 109 2 C30601 IG kappa chain v-I
34 515 70.3 109 2 D30601 IG kappa chain v-I
35 513 70.0 109 2 G30601 IG kappa chain v r
36 513 70.0 116 2 S41917 IG kappa chain v r
37 510 69.6 109 2 PH0963 IG kappa chain v r
38 510 69.6 109 2 F30607 IG kappa chain v-I
39 510 69.6 109 2 F30601 IG kappa chain v-I
40 508.5 69.4 115 1 K3HUVG IG kappa chain pre
41 508 69.3 107 2 PH0965 IG kappa chain v r
42 508 69.3 111 2 S40359 IG kappa chain v-J
43 508 69.3 118 2 T03036 IG light chain - h
44 506.5 69.1 128 2 S40345 IG kappa chain v-J
45 506 69.0 116 1 K3HUVH IG kappa chain pre

ALIGNMENTS

RESULT 1

S49532
anti-Sm antibody VL chain (V kappa 3/5 kappa 2) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49532
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <MAH>
A:Cross-references: EMBL:Z46345; NID:G560843; PIDN:CAA86464.1; PID:G560844
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 630; DB 2; Length 129;

Best Local Similarity 94.5%; Fred. No. 4.7e-43;
Matches 121; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 METPAQLLFLLLLWLPDTTGTEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLFLLLLWLPDTTGTEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFAVYCYCKYGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFAVYCYCKYGTSAITFG 120
Qy 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 2

S20631
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20631
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <LEE>
A:Cross-references: EMBL:Z11903; NID:G33156; PIDN:CAA77955.1; PID:G33157
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>


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Query Match      85.5%; Score 627; DB 2; Length 145;
Best Local Similarity 83.8%; Pred. No. 9e-43;
Matches 119; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120
DB 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120

QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 3
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0022
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 120; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120
DB 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120

QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 4
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0021
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 120; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120
DB 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120

QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 5
S46369
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46369
R:Benisimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <BEN>
A:Cross-references: EMBL:Z27170
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      83.8%; Score 614; DB 2; Length 129;
Best Local Similarity 92.2%; Pred. No. 8.5e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120
DB 61 PQQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEDFAVYCYOKYGTSAITFG 120
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QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 6
S38643
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
R:Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A:Reference number: S38643
A:Accession: S38643
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <BEN>
A:Cross-references: EMBL:Z27170; NID:G415955; PIDN:CAA81694.1; PID:G415956
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-116/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 614; DB 2; Length 134;
Best Local Similarity 92.2%; Pred. No. 8.8e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLFLLWLPTTGTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 6 METPAQVLFLLWLPTTGTGEIVLTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 65

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOKYGTSAITFG 120
Db 66 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPFPFG 125

QY 121 QGTRLEIK 128
Db 126 QGTRLEIK 133

RESULT 7
P10106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P10106; MUID:89235583; PMID:2541221
A:Accession: P10106
A:Molecule type: mRNA
A:Residues: 1-144 <SL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 83.08%; Score 608.5; DB 2; Length 144;
Best Local Similarity 85.2%; Pred. No. 2.6e-41;
Matches 121; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 METPAQLLFLLWLPTTGTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 MEAPAQLLFLLWLPTTGTGEIVLTQSPATLSLSPGERATLSGRASQSV-SSYLAWYQOR 59

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOKYGTSAITFG 120
Db 60 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOQRNWLPTFG 119

QY 121 QGTRLEIKTVAAAPSVFIPPPS 142
Db 120 GGTKEIKRTVAAPSVFIPPPS 141

RESULT 8
S20636
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20636
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20636
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <LEE>
A:Cross-references: EMBL:Z11894; NID:G33200; PIDN:CAA77948.1; PID:G33201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 608; DB 2; Length 128;
Best Local Similarity 91.4%; Pred. No. 2.5e-41;
Matches 117; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 METPAQLLFLLWLPTTGTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLFLLWLPTTGTGEIVLTQSPGTLSPGERATLSGRASQSVSSGYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOKYGTSAITFG 120
Db 61 PQQAPRLIYAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOQYGDSPRTFG 120

QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 9
S40327
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40327
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080691; PMID:8258341
A:Accession: S40327
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72437; NID:G441342; PIDN:CAA51105.1; PID:G441343
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-108/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 596; DB 2; Length 121;
Best Local Similarity 94.2%; Pred. No. 2.1e-40;
Matches 114; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 PAQLLFLLWLPTTGTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOKPGQ 63
Db 1 PAQLLFLLWLPTTGTGEIVLTQSPGTLSPGERATLSGRASQSVSSSYLAWYQOKPGQ 60

QY 64 APRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYOKYGTSAITFGQGT 123
```

[illegible]

RESULT 10

S20637
IG kappa chain v region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20637 S20632
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20637
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <LEE>
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 594; DB 2; Length 130;
Best Local Similarity 89.2%; Pred. No. 3.2e-40;
Matches 116; Conservative 4; Mismatches 8; Indels 2; Gaps 1

QY 1 METPAQLFLLLLWLPDITGEIAITQSPGTLSPGERATISCRASQSFSSYLAWYQOK 60
 |||||
 Db 1 METPAQLFLLLLWLPDITGEIVUTQSPGTLSPGERATISCRASQSLTSNYLAWYQOK 60
 |||||

61 FGOAPBLLIYGASTRATGIPDRFSSGSGTDTLTISRLEPEDFAVYCKYGTG--AIT 118

61 PGQAPRLLYGVSSRATGIPDRFSSASGTFTLTISLEPEDFAVYCOHVGGSPREY 120

QY 119 FGQTRLEIK 128

121 FGQGTKLEIK 130

RESULT 11

A32274
IG kappa chain precursor V-III region (EVI-15) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 30-Sep-1991.#text_change 21-Jan-2000
C:Accession: A32274
R:Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, J.D.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A:Title: Complete protein sequences of the variable regions of the cloned heavy and light
actors of the Wa idiotype family.

A;Reference number: A92767; MUID:88213701; PMID:2452836

A;Accession: A32274
A;Molecule type: DNA
A;Residues: 1-129 <NEW>
A;Cross-references: GB:M20031
A;Note: the authors translated the codon GAT for residue 17 as Ala
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>
F;36-111/Domain: immunoglobulin homology <IMW>

Query Match	80.6%;	Score 591;	DB 2;	Length 129;
Best Local Similarity	89.1%;	Pred. No. 5.6e-40;		
Matches 114.	Conservative	7.	Mismatches	7.
			Index	0.

```

MATCHES 111; CONDUCTIVITY // H2MATCHES // MATCHES // CUFF
OV 1 METPACLELELLLLWL PDDTGEIALTOSPGTSLSPGHRATLSRASOSSESSYLAWYOOK 60

```

1 MEUPAQLLFLLLLWL P DTTGEIIVLTOSP GTLSIPGGERATLS CRASOSVSSNEIAYOOK 60

[illegible]

RESULT. T. 12

S20633
I9: kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C/Accession: S20633
R/Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A/Reference number: S20631
A/Accession: S20633
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-124 <LEE>
A/Cross-references: EMBL:211891; NID:G33185; PID:CAA77945.1; PID:G33186
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:32-107/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 576; DB 2; Length 124;
Best Local Similarity 88.7%; Pred. No. 8.2e-33;
Matches 110; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 5 AQLFLLLLWLPD TTGEIALTQSPGTLSLSPGERATLS CRASQSFSSYLAWYQOKPGQA 64

Db 1 AQLFLLLWLPLDITGEIVLTQSPGTLSPGERATLSCRASQSYSLAWIQKPGQA 60

Qy 65 PRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFANVYQCXYGTSALTGQGR 124

Db 61 PRLIIGTSSRATGIPDRVSGSGGDTFLTISRLEPEDFAMYYCQQYGSSSYTFGGTK 120

QY 125 LEIK 128
III:

Db 121 LEIR 124

RESULT 13
B27594
IG kappa chain precursor V-III (Nalm-6) - human
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988#sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: B27594
R:Granger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.
J. Exp. Med. 167, 488-501, 1988
A:Title: The kappa-deleting element. Germ-line and rearranged, duplicated and dispersed
A:Reference number: A92779; MUID:88154739; PMID:3126251
A:Accession: B27594
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-116 <GRA>
A>Note: this sequence was translated from an aberrantly rearranged kappa gene from lam.
C:Genetics:

A;Map position: 2
A; Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F1-20/Domain: signal sequence #status predicted <SIG>
F1-36-111/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 574; DB 2; Length 116;

Best Local Similarity 95.7%; Pred. NO. 1.1e-38;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 METPAQLLFLLLLWLPDTTGRIALTQSPCTLSLSPGERATLSGRASQSFSSSYLAWYQQK 60

Db

1

MEIPAQLFLLLLWLPDPTTGEIVLVTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK

60

QY

61

PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYKGTG

115

Db

61

PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYKGTG

115

RESULT 14

S40346

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40346

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40346

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: EMBL:X72456; NID:G441380; PIDN:CAA51124.1; PID:G441381

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-110/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 567.5; DB 2; Length 131;

Best Local Similarity 85.5%; Pred. No. 4e-38;

Matches 112; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY

2

ETPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOKP

61

Db

1

ETPAQLFLLLLWLPDPTTGEIVLVTQSPGTLSPGERATLSCRASQSVSSYLAWYQHP

60

QY

62

GOAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYKGTG

120

Db

61

GOAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCHYKGGSPPTFG

120

QY

121

QGTREIKGTV

131

Db

121

QGTREIKRTV

131

RESULT 15

S40325

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40325

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40325

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:Cross-references: EMBL:X72435; NID:G441338; PIDN:CAA51103.1; PID:G441339

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-110/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 563.5; DB 2; Length 129;

Best Local Similarity 82.8%; Pred. No. 8.2e-38;

Matches 106; Conservative 14; Mismatches 7; Indels 1; Gaps 1;

QY

2

ETPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOKP

61

Db

1

ETPAQLFLLLLWLPDTPGQVLVTQSPGTLSPGERATLSCRASQSVSGSYLAWYQORP

60

QY

62

GOAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYKGTSAI

120

Db

61

GOAPRLIIYGASTRATGVPDRFSGSGGTDFTLTISRMEPEDFAVYYCQYGGSPPLTFG

120

QY

121

QGTREIK

128

Db

121

PGTKVDIR

128

Search completed: April 5, 2004, 13:43:02

Job time : 12.533 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.48731 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLLELLMLPDTTG.....TRLEIKGTVAAPSVFIIPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	85.1	129	1 KV3L_HUMAN	P18135 homo sapien
2	614	83.8	129	1 KV3M_HUMAN	P18136 homo sapien
3	557.5	76.1	128	1 KV3K_HUMAN	P06311 homo sapien
4	537	73.3	129	1 KV3H_HUMAN	P04207 homo sapien
5	508.5	69.4	115	1 KV3J_HUMAN	P04433 homo sapien
6	506	69.0	116	1 KV3J_HUMAN	P04434 homo sapien
7	505	68.9	109	1 KV3B_HUMAN	P01620 homo sapien
8	502	68.5	109	1 KV3E_HUMAN	P01623 homo sapien
9	498	67.9	109	1 KV3D_HUMAN	P01622 homo sapien
10	489	66.7	108	1 KV3A_HUMAN	P04206 homo sapien
11	482	65.8	109	1 KV3G_HUMAN	P01619 homo sapien
12	466	63.6	100	1 KV3C_HUMAN	P01621 homo sapien
13	447	61.0	109	1 KV3F_HUMAN	P01624 homo sapien
14	427.5	58.3	129	1 KV1W_HUMAN	P04431 homo sapien
15	420.5	57.4	134	1 KV4C_HUMAN	P06314 homo sapien
16	413	56.3	133	1 KV4B_HUMAN	P06313 homo sapien
17	404.5	55.2	117	1 KV1J_HUMAN	P01602 homo sapien
18	399.5	54.5	131	1 KV4J_HUMAN	P01661 mus musculus
19	395.5	54.0	114	1 KV4A_HUMAN	P01625 homo sapien
20	394	53.8	133	1 KV2F_HUMAN	P06310 homo sapien
21	390.5	53.3	132	1 KV3F_HUMAN	P01658 mus musculus
22	381.5	52.0	108	1 KV1H_HUMAN	P01600 homo sapien
23	380.5	51.9	108	1 KV1M_HUMAN	P01605 homo sapien
24	379.5	51.8	121	1 KV4O_HUMAN	P06312 homo sapien
25	379.5	51.8	129	1 KV1X_HUMAN	P04432 homo sapien
26	378.5	51.6	128	1 KV5E_MOUSE	P01637 mus musculus
27	376.5	51.4	108	1 KV1F_HUMAN	P01598 homo sapien
28	376.5	51.4	108	1 KV1Q_HUMAN	P01609 homo sapien
29	370.5	50.5	149	1 KV5A_MOUSE	P01633 mus musculus
30	369.5	50.4	108	1 KV1Y_HUMAN	P080362 homo sapien
31	366	49.9	107	1 KV1D_HUMAN	P01596 homo sapien
32	365.5	49.9	108	1 KV1L_HUMAN	P01604 homo sapien
33	365.5	49.9	108	1 KV1V_HUMAN	P04430 homo sapien

RESULT 1

KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988)
RL -1- DISEASE: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.
CC PIR; P10022; K3HUHA.
CC HSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_Like; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 UKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

ALIGNMENTS

Query Match 85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.3e-53;
Matches 129; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 METPAQLLELLMLPDTTGTEALTSQPTLSLSPGERATLSQASQSSSYLAWYQOK 60

Db 1 METPAQLLELLMLPDTTGTEALTSQPTLSLSPGERATLSQASQSSSYLAWYQOK 60

Qy 61 PGQAPRLIYGASTRAIGIPDRFSGSGSGCTDFTLTISRLEPEDPAVYVYQKYGTSAITFG 120

```
Db 61 PQQAPRLIYGCSSRATGIDRFSGSGSGDFTLTISRLEPEDFAVYCCQYGTSPRTFG 120
QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 2
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P8136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RX Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RA "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P00021; K3HUH1.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 FRAMEWORK-3.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 7395528EA2BB74D6 CRC64;

Query Match 83.8%; Score 614; DB 1; Length 129;
Best Local Similarity 92.2%; Pred. No. 1.2e-52;
Matches 118; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAHYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAHYQOK 60
QY 61 PQQAPRLIYGCSSRATGIDRFSGSGSGDFTLTISRLEPEDFAVYCCQYGTSAITFG 120
Db 61 PQQAPRLIYGCSSRATGIDRFSGSGSGDFTLTISRLEPEDFAVYCCQYGTSAITFG 120
QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 3
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
```

```
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86041852; PubMed=2997711;
RX Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RA "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00021; CRA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 76.1%; Score 557.5; DB 1; Length 128;
Best Local Similarity 86.7%; Pred. No. 3.6e-47;
Matches 111; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAHYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAHYQOK 59
QY 61 PQQAPRLIYGCSSRATGIDRFSGSGSGDFTLTISRLEPEDFAVYCCQYGTSAITFG 120
Db 60 RQGPRLIIRPSSRANGIPDRFSGSGSGDFTLTISRLEPEDFAVYCCQYGTSAITFG 119
QY 121 QGTRLEIK 128
Db 120 QGTRLEIK 127

RESULT 4
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
```

DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region C_{LL} precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177570; PubMed=3083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M12740; AAAS8992.1; --
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION C_{LL}.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 109 118 FRAMEWORK-3.
 FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 JK1 SEGMENT.
 FT NON_TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
 Query Match 73.3%; Score 537; DB 1; Length 129;
 Best Local Similarity 82.9%; Pred. No. 3.6e-45;
 Matches 107; Conservative 8; Mismatches 12; Indels 2; Gaps 2;
 QY 1 METPAQLFLLLMLPDTTGTGIALTQSPGTLSPGERATLSCEASQSFSSSYLAWYQOK 60
 DB 1 MEAPAQFLFLLLMLPDTTGTGIVNTQSPATLSVSPGERATLSCEASQSVNN-LAWYQOK 59
 QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTFTLTISRLEPEDFAVYCYGKT-SAITF 119
 DB 60 PQQAPRLIYGASTRATGIPARFSGSGGTFTLTISRLOSEDFAVYCCQYNNWPPWTF 119
 QY 120 GQTRLEIK 128
 DB 120 GQTRVEIK 128
 RESULT 5
 ID KV3J_HUMAN STANDARD; PRT; 115 AA.
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus."
 RL Nucleic Acids Res. 12:9229-9236(1984).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X01668; --; NOT ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 109 115 FRAMEWORK-3.
 FT DOMAIN 115 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
 Query Match 69.4%; Score 508.5; DB 1; Length 115;
 Best Local Similarity 91.0%; Pred. No. 1.8e-42;
 Matches 101; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
 QY 1 METPAQLFLLLMLPDTTGTGIALTQSPGTLSPGERATLSCEASQSFSSSYLAWYQOK 60
 DB 1 MEAPAQFLFLLLMLPDTTGTGIVNTQSPATLSVSPGERATLSCEASQSV-SSYLAWYQOK 59
 QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTFTLTISRLEPEDFAVYCYOK 111
 DB 60 PQQAPRLIYGASTRATGIPARFSGSGGTFTLTISRLEPEDFAVYCYOQ 110
 RESULT 6
 ID KV3J_HUMAN STANDARD; PRT; 116 AA.
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;

```
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus";
CC Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02725; -, NOT ANNOTATED_CDS.
DR PIR; A01901; K3HUVH.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 69.0%; Score 506; DB 1; Length 116;
Best Local Similarity 88.3%; Pred. No. 3.2e-42;
Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 METPAQLFLLLWLPDTHGIALTQSPGTLSLSPGERATLSCRASQSFSSYLAWYQOK 60
DB 1 MEAPAQLLFLLLWLPDTHREIVMTQSPPTLSLSPGERVTLSCRASQSVSSYLTYQOK 60
QY 61 PQCAPRLTYGASTRATGIPORFSGSGGTDFTLTISLPLEDFAVYCYQK 111
DB 61 PQCAPRLTYGASTRATGIPARFSGSGGTDFTLTISLPLEDFAVYCYQK 111

RESULT 7
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HUVL.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 68.5%; Score 502; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 7.2e-42;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSLSPGERATLSCRASQSFSSYLAWYQOKPQAPRLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLWYQKPGQAPRLIYGASSRATGIP 60
QY 81 DRFGSGSGGTDFTLTISLPLEDFAVYCYQKYGTSAITFGQTRLEIK 128
DB 61 DRFGSGSGGTDFTLTISLPLEDFAVYCYQYQSGSPQTFGQSGKVEIK 108

RESULT 8
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region WOL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HUVL.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3EC6D46FFB4 CRC64;

Query Match 68.9%; Score 505; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 3.7e-42;
Matches 96; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSLSPGERATLSCRASQSFSSYLAWYQOKPQAPRLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLWYQKPGQAPRLIYGASSRATGIP 60
QY 81 DRFGSGSGGTDFTLTISLPLEDFAVYCYQKYGTSAITFGQTRLEIK 128
DB 61 DRFGSGSGGTDFTLTISLPLEDFAVYCYQYQSGSPQTFGQSGKVEIK 108
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RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus";
CC Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC -----
CC EMBL; X02725; -, NOT ANNOTATED_CDS.
DR PIR; A01901; K3HUVH.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 69.0%; Score 506; DB 1; Length 116;
Best Local Similarity 88.3%; Pred. No. 3.2e-42;
Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 METPAQLFLLLWLPDTHGIALTQSPGTLSLSPGERATLSCRASQSFSSYLAWYQOK 60
DB 1 MEAPAQLLFLLLWLPDTHREIVMTQSPPTLSLSPGERVTLSCRASQSVSSYLTYQOK 60
QY 61 PQCAPRLTYGASTRATGIPORFSGSGGTDFTLTISLPLEDFAVYCYQK 111
DB 61 PQCAPRLTYGASTRATGIPARFSGSGGTDFTLTISLPLEDFAVYCYQK 111

RESULT 7
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
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DB 61 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSLGRITFGQGTKEIK 108
|||||
RESULT 9
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID KV3D_HUMAN
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Sevler's Z. Physiol. Chem. 353:189-208 (1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23
FT NON TER 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDDC7749BC CRC64;

Query Match 67.9%; Score 498; DB 1; Length 109;
Best Local Similarity 88.0%; Pred. No. 1.7e-41;
Matches 95; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
|||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLIYVASSRATGIP 60
|||||
QY 81 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSLGRITFGQGTKEIK 128
|||||
DB 61 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSPSTFGQGTKEIK 108
|||||

RESULT 10
KV3A_HUMAN STANDARD; PRT; 108 AA.
ID KV3A_HUMAN
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX Milstein C.;
RA "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6."
RL FEBS Lett. 2:301-304 (1969).
```

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CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23
FT NON TER 108
FT BY SIMILARITY.
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 66.7%; Score 489; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 1.3e-40;
Matches 89; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
|||
DB 1 ZIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYSGSPSTFGQGTKEIK 60
|||||
QY 81 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSLGRITFGQGTKEIK 128
|||||
DB 61 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSPSTFGQGTKEIK 108
|||||

RESULT 11
KV3G_HUMAN STANDARD; PRT; 109 AA.
ID KV3G_HUMAN
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies."
RL Mol. Immunol. 23:239-244 (1986).
DR PIR; A01893; K3HUGO.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23
FT NON TER 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 65.8%; Score 482; DB 1; Length 109;
Best Local Similarity 85.2%; Pred. No. 6.2e-40;
Matches 92; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
|||
DB 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYSGSPSTFGQGTKEIK 60
|||||
QY 81 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSLGRITFGQGTKEIK 128
|||||
DB 61 DRFSGSGSDFTLTISRLEPEDFAVYCCQYSGSPSTFGQGTKEIK 108
|||||
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```
RESULT 12
KV3C HUMAN
ID KV3C HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes."
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 27 93
FT NON TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363C52632F CRC64;

Query Match 63.6%; Score 466; DB 1; Length 100;
Best Local Similarity 91.8%; Pred. No. 2e-38;
Matches 89; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 19 TGETALQSPGTLSPGERATLSGRATLSRLEPEDFAVYCYQKGTGTS 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 SGEIVLTQSPGTLSPGERATLSGRATLSRLEPEDFAVYCYQKGTGTS 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 79 IPDRFSGSGGTDTLTISRLPEDEFAVYCYQKGTGTS 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 IPDRFSGSGGTDTLTISRLPEDEFAVYCYQKGTGTS 99
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
KV3F HUMAN
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IgM anti-gamma globulins."
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
FT CHAIN 1 22
FT DOMAIN 23 129
FT DOMAIN 46 56
FT DOMAIN 57 71
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8A86 CRC64;

Query Match 61.0%; Score 447; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.5e-36;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSGRATLSRLEPEDFAVYCYQKGTGTS 128
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVMTQSPVTLSPGERATLSGRATLSRLEPEDFAVYCYQKGTGTS 108
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 DRFGSGSGGTDTLTISRLPEDEFAVYCYQKGTGTS 128
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ARFGSGSGGTDTLTISRLPEDEFAVYCYQKGTGTS 108
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
KV1W HUMAN
ID KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04331;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
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or send an email to license@isb-sib.ch).
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUNK.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 46 56
FT DOMAIN 57 71
SQ SEQUENCE 129 AA; 14922 MW; 62821DDC6A8A86 CRC64;
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FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 58.3%; Score 427.5; DB 1; Length 129;
Best Local Similarity 56.4%; Pred.No.1.4e-34;
Matches 85; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 METPAQLLLFLLMLPDTTGEIALTQSPGTLSPGERATLSRASQSFSSSYLA 60
Db 3 MRVPAQLLLGILLWLRGARDIQMTQSPSLASVGRVTITCRASQSI-SNYLWYQOK 61

QY 61 PGQAPRLLYGASTRATGIPDRFSGSGSGTDFLTLSRLEPEDFAVYCYOKYGTSAITFG 120
Db 62 PGKAPKLLIYAASSLQSGVTSRFSGSGSGTDFLTLSLQPEDSATYICQSYSTLITFG 121

QY 121 QGTRLEIK 128
Db 122 QGTRLEIK 129

RESULT 15
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RA Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02990; CAA26733.1; -
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; IG; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 20 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 134 FRAMEWORK-1.
FT DOMAIN 21 43 FRAMEWORK-2.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
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FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 57.4%; Score 420.5; DB 1; Length 134;
Best Local Similarity 60.9%; Pred.No.7.1e-34;
Matches 81; Conservative 20; Mismatches 27; Indels 5; Gaps 1;

QY 1 METPAQLLLFLLMLPDTTGEIALTQSPGTLSPGERATLSRASQSFSSSYLA 55
Db 1 MVLQTVFISILLWISGAYGDIWVTQSPDSLAVSLGERATINCKSSQSIYSSDNKNYLA 60

QY 56 WYQOKPQAPRLLYGASTRATGIPDRFSGSGSGTDFLTLSRLEPEDFAVYCYOKYGTSAITFG 115
Db 61 WYQOKPQAPRLLYGASTRATGIPDRFSGSGSGTDFLTLSRLEPEDFAVYCYOKYGTSAITFG 120

QY 116 AITFGQTRLEIK 128
Db 121 PWTEGQTKVEIK 133
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Search completed: April 5, 2004, 13:24:55
Job time : 6.48731 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 30.2741 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLFLLLWLPDTTG.....TRLEIKGTVAPEVFIFPPS 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL 25:*

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_phase:*

11: sp_plant:*

12: sp_rodent:*

13: sp_virus:*

14: sp_vertebrate:*

15: sp_unclassified:*

16: sp_rvirus:*

17: sp_bacteriap:*

18: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	68.9	109	4 Q9UL78	Q9UL78 homo sapien
2	495.5	67.6	234	4 Q7A473	Q7A473 homo sapien
3	491	67.0	109	4 Q9UL66	Q9UL66 homo sapien
4	473.5	64.6	236	4 Q7Z3Y4	Q7Z3Y4 homo sapien
5	466	63.6	239	4 Q8NEKO	Q8NEKO homo sapien
6	450	61.4	239	4 Q8TCDO	Q8TCDO homo sapien
7	425.5	58.0	237	13 Q7SZ36	Q7SZ36 xenopus lae
8	424.5	57.9	108	4 Q9UL63	Q9UL63 homo sapien
9	422	57.6	109	4 Q9UL65	Q9UL65 homo sapien
10	413.5	56.4	236	11 Q7TWK3	Q7TWK3 mus musculus
11	413.5	56.4	238	11 Q9N437	Q9N437 mus musculus
12	412.5	56.3	236	11 Q7TS98	Q7TS98 mus musculus
13	406.5	55.5	238	11 Q8VCT16	Q8VCT16 mus musculus
14	405.5	55.3	234	11 Q8VCP0	Q8VCP0 mus musculus
15	390	53.2	239	11 Q8VC55	Q8VC55 mus musculus
16	389.5	53.1	234	11 Q8R062	Q8R062 mus musculus

17	385	52.5	239	11 Q8KOF8	Q8KOF8 mus musculus
18	382.5	52.2	108	4 Q9UL70	Q9UL70 homo sapien
19	382.5	52.2	234	11 Q9LW8	Q9LW8 mus musculus
20	381.5	52.0	108	4 Q9UL79	Q9UL79 homo sapien
21	380.5	51.9	108	4 Q9UL77	Q9UL77 homo sapien
22	377	51.4	107	4 Q9ESA9	Q9ESA9 homo sapien
23	370.5	50.5	131	11 Q8L1C3	Q8L1C3 mus musculus
24	366.5	50.0	214	11 Q9RIA5	Q9RIA5 mus musculus
25	364	49.7	114	11 Q8KIF1	Q8KIF1 mus musculus
26	362	49.4	107	4 Q9UL81	Q9UL81 homo sapien
27	360.5	49.2	116	4 Q9EP86	Q9EP86 homo sapien
28	360.5	49.2	233	11 Q9LW89	Q9LW89 mus musculus
29	360	49.1	235	11 Q9LW12	Q9LW12 mus musculus
30	359	49.0	235	11 Q7TMK0	Q7TMK0 mus musculus
31	345	47.1	112	11 Q8KIF2	Q8KIF2 mus musculus
32	342.5	46.7	298	11 Q9QVFO	Q9QVFO mus musculus
33	342	46.7	112	11 Q8KIF3	Q8KIF3 mus musculus
34	341.5	46.6	111	11 Q92OE9	Q92OE9 mus musculus
35	338.5	46.2	107	11 Q9ERZ3	Q9ERZ3 mus musculus
36	335.5	45.8	148	11 Q8K122	Q8K122 mus musculus
37	334	45.6	106	5 Q9U410	Q9U410 schistosoma
38	333.5	45.5	127	11 Q925S9	Q925S9 mus musculus
39	332	45.3	134	11 Q8VDD0	Q8VDD0 mus musculus
40	330.5	45.1	109	11 Q92OB6	Q92OB6 mus musculus
41	330.5	45.1	234	11 Q8R028	Q8R028 mus musculus
42	328.5	44.8	111	11 Q8L1U6	Q8L1U6 mus musculus
43	321.5	43.9	99	11 Q9JL74	Q9JL74 mus musculus
44	320.5	43.7	108	11 Q8V1J0	Q8V1J0 mus musculus
45	319	43.5	243	11 Q7TQM2	Q7TQM2 mus musculus

ALIGNMENTS

RESULT 1
Q9UL78
ID Q9UL78 PRELIMINARY; PRT: 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.

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DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 68.9%; Score 505; DB 4; Length 109;
Best Local Similarity 89.8%; Pred. No. 1.1e-44; Indels 0; Gaps 0;
Matches 97; Conservative 6; Mismatches 5;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDCAVYCCYQYGSPLTFGGTKVEIK 108

RESULT 2
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 67.6%; Score 495.5; DB 4; Length 234;
Best Local Similarity 69.0%; Pred. No. 3e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCYQYGSIFTFGGTKVDIK 108

Query Match 67.0%; Score 491; DB 4; Length 109;
Best Local Similarity 87.0%; Pred. No. 3.2e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCYQYGSIFTFGGTKVDIK 108

RESULT 4
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 109
FT NON TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 67.0%; Score 491; DB 4; Length 109;
Best Local Similarity 87.0%; Pred. No. 3.2e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCYQYGSIFTFGGTKVDIK 108

RESULT 4
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 109
FT NON TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 67.0%; Score 491; DB 4; Length 109;
Best Local Similarity 87.0%; Pred. No. 3.2e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCYQYGSIFTFGGTKVDIK 108
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```
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC005332; AAH05332.1; -.
DR Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBPE4ED23084BC6 CRC64;

Query Match 64.6%; Score 473.5; DB 4; Length 236;
Best Local Similarity 65.5%; Pred. No. 5.8e-41;
Matches 93; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

QY 1 METPAQLFLILLMLPDTTGEIALTQSPGTLISLSPGERATLSCRASQSPSSYLAWYQOK 60
Db 3 MRVLAQLGLLLLCFFGARCIDIQWTQSPSSLSASVGTVTITCRASQDI-SNYLAWFQOK 61

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYCYQKYGTS 120
Db 62 PGKAPKSLIYGASSLQSGVSKFSGSGSGTDFLTISRLEPEDFAVYCYQKYGTS 121

QY 121 QGTREIKGTVAAPSVFIFFPS 142
Db 122 QGTREIKRTVAAPSVFIFFPS 143

RESULT 5
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC022362; AAH22362.1; -.
DR PIR; S34095; S34095.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
RW FASEB J. 17:26024 (2002).
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 61.4%; Score 450; DB 4; Length 239;
Best Local Similarity 58.9%; Pred. No. 1.6e-38;
Matches 86; Conservative 27; Mismatches 29; Indels 4; Gaps 1;

QY 1 METPAQLFLILLMLPDTTGEIALTQSPGTLISLSPGERATLSCRASQSPSSYLAW 56
Db 1 MRVLAQLGLLLMLVFGSGSGTDFLTISRLEPEDFAVYCYQKYGTS 60

QY 57 YQKPGQAPRLIYGASTRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYCYQKYGTS 116
Db 61 FQQRPGQSPRLIYKVSNRDGVDPDRFSGSGSGTDFLTISRLEPEDFAVYCYQKYGTS 120

QY 117 ITFGQGTREIKGTVAAPSVFIFFPS 142
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D_b 121 STFGGTKLEIKRTVAAPSVFIFPPS 146

RESULT	7
ID	Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC	Q7SZ36;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypotheical protein.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Ampibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]_TaxID=8355;
RP	SEQUENCE FROM N.A.
RC	TISSUE=Whole;
RX	MEDLINE=22341132; PubMed=12454917;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.;
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT	initiative.";
RL	Dey. Dyn. 225:384-391(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Whole;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
EA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodríguez A.C., Grimwood J., Schmütz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marza M.A.
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Whole;
RA	Klein S., Strausberg R.;
RE	Submitted (JUN-2003) to the ENMBL/GenBank/DDBJ databases.
DR	ENMBL; BC054155; AAAH54155.1; -;
KW	Hypothetical protein.
SQ	SEQUENCE 237 AA; 26300 MW; 47B8D0D2639C436 CRC64;
Query Match . 58.0%; Score 425.5; DB 13; Length 237;	
Best Local Similarity 61.2%; Pred No. 5.6e-36;	
Matches 85; Conservative 20; Mismatches 31; Indels 3; Gaps 1	
Qy	7 LPFLLLMLPDDTTGGIATQTSPGTLSUGGERATLSGRASGSP---SSSYLAWYQQKPKQ 63 ::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Db	7 LLPILMLMGSGYGIVLTQSPPDYVSVSFGETVTITCKASSVAIGSTLYLHWYQQKSQG 66 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Qy	64 APPELLYAGSTRATGPDRFSGSGSDTFTLTISRLEPEDPVAVYCGKYGTSAITFGQOT 123 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Db	67 VPKLLEYLANTRHTGTPRISGSOGSDTFTLTISRMEAEADAAAYCYQSRSDPLTFKGKT 126 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Qy	124 RLSEIKGTVAAPSVFIIPPS 142 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Db	127 RVELKENDAKPAVFIFKPS 145 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :

RESULT 8

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Q9UL83 PRELIMINARY; PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RX Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL, AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IGLIKE; 1.
FT NON TER 1
FT FT 108
FT NON TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96BEA CRC64;

Query Match 57.9%; Score 424.5; DB 4; Length 108;
Best Local Similarity 78.7%; Pred.No. 2.5e-36;
Matches 85; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 21 EIALTOSPGLTSLSPGERATLSCRASQSFSSSYLAWYQQPGQAPELLIYGASTRATGIP 80
Db 1 EIWMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQPGQAPELLIYGASTRATGIP 59
Qy 81 DRPSGGSGGDFTLTTSRLPEPDFAVYYCKYGTSAITFGQGRLK 128
Db 60 ARFSGGSGGFTEFLTISSLQPEDFAVYYCHYNWFPTFGTKVDIK 107

RESULT 9
Q9UL85 PRELIMINARY; PRT; 109 AA.
ID Q9UL85
AC Q9UL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RX Clin. Immunol. Immunopathol. 87:184-192(1998).

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DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSSP; P80362; 1WT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1B43ETC7AFACCC CRC64;

Query Match 57.6%; Score 422; DB 4; Length 109;
Best Local Similarity 77.1%; Pred. No. 4.7e-36;
Matches 84; Conservative 12; Mismatches 11; Indels 2; Gaps 2;

QY 21 EIALTSPGTLSPGERATLSRCASQSPSSSVLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVYTSPTLSVSPGERATLSRCASQSSSN-LAWYQKPGQAPRLIYGASTRATGIP 59
QY 81 DRFSGSGGDTFTLTSRLEPEFPAVYQKYGCT-SAITFGGQTRLEIK 128
Db 60 ARFSGSGGTEFTLTISSQSEDFAIYHCQYNSWPELFGGQTKVEIK 108

RESULT 10
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 56.4%; Score 413.5; DB 11; Length 238;
Best Local Similarity 54.8%; Pred. No. 1e-34;
Matches 80; Conservative 28; Mismatches 33; Indels 5; Gaps 2;

QY 1 METPAQLLFLLLWLPDTTGTGIALTQSPGTLSPGERATLSRCASQSPSSSVLAWYQOK 60
Db 3 MRAPAQFGILLWLPFGIRCDIKMTQSPSSMYASLGSRVITCKASODI-KSYLSWYQOK 61
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGDTFTLTSRLEPEFPAVYQKYGCTSAITFG 120
Db 62 PWKSPKTLIYATSLADGVSRFSGSGGQDYSLTISSLESDDTATYCYCLQHGESPTFG 121
QY 121 QGTRLEIKGTVAAPSVFIFPPS 142
Db 122 SGTKEIKRADAAFTVSIFPPS 143

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 56.4%; Score 413.5; DB 11; Length 238;
Best Local Similarity 54.8%; Pred. No. 1e-34;
Matches 80; Conservative 28; Mismatches 33; Indels 5; Gaps 2;

QY 1 METPAQLLFLLLWLPDTTGTGIALTQSPGTLSPGERATLSRCASQSPSSSVLAWYQOK 60
Db 1 MKLPVRL-LVLMFWIPASSDVMVTQTPLSLPVLGQASISCRSSQSIHVSNGNTYLEW 59
QY 57 YQKPGQAPRLIYGASTRATGIPDRFSGSGGDTFTLTSRLEPEFPAVYQKYGCTSA 116
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Db 60 YLQKPGQSKLLIYKVNRFSGVDRFSGSGGTDFTLKISRVEADLGVYCFQGSHPV 119
QY 117 ITFGQGTREIKGTVAAPSVFIPEPS 142
Db 120 YTFGSGTKLEIKRADAAPTVSIPEPS 145

RESULT 12
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=9372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB29160.1; -.
SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

Query Match 56.3%; Score 412.5; DB 11; Length 236;
Best Local Similarity 56.3%; Pred. No. 1.3e-34;
Matches 80; Conservative 22; Mismatches 39; Indels 1; Gaps 1;

QY 1 METPAQLFLLLMLPDTTGIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
Db 3 MRPQFLGILLWFPQMKCDIKMTQSPSMYASLGERVTITCKASQDI-NSYLSWFQOK 61
QY 61 PQQAPRLIYGASTRATGIDPRFSGSGGTDFLTITSLRLEPDEFVAVYCKYGTSAITFG 120
Db 62 PKSKPKLIYRANFLVDGVSFRFSGSGGQDYSLTISLVEDMGVIYCLQYDEFRTFG 121
QY 121 QGTREIKGTVAAPSVFIPEPS 142
Db 122 GGTLEIKRADAAPTVSIPEPS 143

RESULT 13
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.

Query Match 55.5%; Score 406.5; DB 11; Length 238;
Best Local Similarity 54.1%; Pred. No. 5.3e-34;
Matches 79; Conservative 29; Mismatches 33; Indels 5; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGIALTQSPGTLSPGERATLSGRASQSFSSSYLAW 56
Db 1 MKLPVRLI-VLMFWIPASSSDVMTQTLPLVPLGDAQISCRSSQSLVHSGNTYLHW 59
QY 57 YQKPGQAPRLIYGASTRATGIDPRFSGSGGTDFLTITSLRLEPDEFVAVYCKYGTSA 116
Db 60 YLQKPGQSKLLIYKVNRFSGVDRFSGSGGTDFTLKISRVEADLGVYCFQGSHPV 119
QY 117 ITFGQGTREIKGTVAAPSVFIPEPS 142
Db 120 PTFGGTKLEIKRADAAPTVSIPEPS 145

RESULT 14
Q8VCPO PRELIMINARY; PRT; 234 AA.
AC Q8VCPO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
```

Search completed: April 5, 2004, 13:42:05
Job time : 32.2741 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:09:21 ; Search time 45.9917 Seconds
(without alignments)
874.270 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 MPTPQLFLLLLLLWLPDTTG.....TRLEIKGTVAAPSVFIFFPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	733	100.0	142	4	AAB47060 Light cha
2	733	100.0	142	5	AAOI8877 Human B02
3	682	93.0	235	3	AAV93702 The kappa
4	682	93.0	235	3	AAV93729 The kappa
5	682	93.0	235	6	AAE35884 Human 4.1
6	666	90.9	235	6	ABP71366 Anti-OPGL
7	658.5	89.8	234	7	ADZ28481 Human ant
8	658.5	89.8	234	5	AAU74299 Anti-huma
9	654.5	89.3	143	4	AAB47061 Light cha
10	654.5	89.3	143	5	AAOI8879 Human KRI
11	654	89.2	233	3	AAV93704 The kappa
12	654	89.2	233	3	AAV93731 The kappa
13	654	89.2	233	6	AAE35886 Human 4.8
14	653.5	89.2	236	5	AAU74301 Anti-huma
15	650.5	88.7	234	3	AAV93733 The kappa
16	650.5	88.7	234	3	AAV93708 The kappa
17	650.5	88.7	234	6	AAE35888 Human 6.1
18	649	88.5	150	2	AAW40069 Human mon
19	649	88.5	150	4	AAE00946 Human mon
20	641	87.4	150	7	ABU10485 Human C-a
21	636	86.8	130	6	ABJ36930 Anti-CD40
22	633.5	86.4	234	3	AAV92239 Human bon
23	627.5	85.6	234	7	ADZ28473 Human ant
24	625	85.3	129	2	AAR38672 VK325-JK2
25	624.5	85.2	134	2	AAW11155 Anti-lung

ALIGNMENTS

RESULT 1
AAB47060
ID AAB47060 standard; protein; 142 AA.
XX AC AAB47060;
XX
DT 08-MAY-2001 (first entry)
XX
DE Light chain variable region VL of B02C11.
XX
KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;
KW complementarity determining region; CDR; MAb; B02C11;
KW conformational epitope; factor VIII; KR1X1; von Willebrand factor;
KW hemostasis; intravascular coagulation; arterial thrombosis;
KW arterial restenosis; venous thrombosis; arteriosclerosis.
XX OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 43..54
FT /label= CDR1
FT Domain 69..75
FT /label= CDR2
FT Domain 109..117
FT /label= CDR3
XX WO200104269-A1.
XX 18-JAN-2001.
XX 13-JUL-2000; 2000WO-EP006677.
XX 14-JUL-1999; 99GB-00016450.
XX 14-JUL-1999; 99US-0143891P.
XX (LEUV-) LEUVEN RES & DEV VZW.
XX Jacquemin MG, Saint-Remy JR;
XX WPI; 2001-138333/14.
XX N-FSDB; AAC85453.
XX Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
XX Example 5; Fig 7; 55pp; English.
XX

26 620.5 84.7 131 6 ABP57366 Anti-TPAI
27 615 83.9 238 6 ABR41582 Human DIT
28 614 83.8 130 6 ADA43061 Human ant
29 602 82.1 129 2 AAR38673 F105Vb-F1
30 602 82.1 129 2 AAR41286 F105 rear
31 601 82.0 235 7 ADD01357 Human imm
32 600.5 81.9 236 4 AAG71272 Human gen
33 600.5 81.9 236 5 ABG63490 Human alb
34 596 81.3 128 7 ADC61062 Human ant
35 593 80.9 384 4 AAM24101 Human EST
36 592.5 80.8 234 2 AAR52951 Human ant
37 592 80.8 124 2 AAW24539 Immunoglob
38 590 80.5 384 4 AAU14462 Human nov
39 590 80.5 384 4 AAU14463 Human nov
40 590 80.5 384 4 AAU14461 Human nov
41 590 80.5 384 4 AAU14464 Human nov
42 589.5 80.4 234 5 AAO14066 Light cha
43 589.5 80.4 234 6 ABU08018 Human mon
44 583 79.5 178 4 AAU33249 Novel hum
45 574 78.3 116 2 AAR38650 Human V-k

CC This sequence represents the light chain variable region of the human
 CC monoclonal antibody (MAB), B02C11. B02C11 is a human MAB which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg2150His factor
 CC VIII light chains. The MAB produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X 1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC haemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 XX
 XX SQ Sequence 142 AA;

Query Match 100.0%; Score 733; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.9e-42;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLISLSPGERATLSCEASQSFSSSYLAWYQOK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLISLSPGERATLSCEASQSFSSSYLAWYQOK 60
 QY 61 PQQAPRLIYGASTRATGIDPRFSGSGSDFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 DB 61 PQQAPRLIYGASTRATGIDPRFSGSGSDFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 QY 121 QGTRLEIKGTVAAPSVFIFFPS 142
 DB 121 QGTRLEIKGTVAAPSVFIFFPS 142

RESULT 2
 AAO18877
 ID AAO18877 standard; protein; 142 AA.

XX AAO18877;
 XX 07-NOV-2002 (first entry)
 DT
 DE Human B02C11 light chain variable region.

XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antinflammatory.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Region 43..54
 FT /label= CDR1
 FT Region 69..75
 FT /label= CDR2
 FT Region 108..116
 FT /label= CDR3

EP1222929-A2.

17-JUL-2002.

11-JAN-2002; 2002EP-00447005.

11-JAN-2001; 2001US-0261405P.

(COLL-) COLLEN RES FOUND VZW D.

Jacquemin MG, Saint-Remy JR;

XX WPI; 2002-610270/66.
 DR N-PSDB; AAL49255.
 XX
 PT Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.
 XX
 PS Disclosure; Fig 11; 41pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the light chain variable region of B02C11
 XX
 XX SQ Sequence 142 AA;

Query Match 100.0%; Score 733; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.9e-42;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLISLSPGERATLSCEASQSFSSSYLAWYQOK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLISLSPGERATLSCEASQSFSSSYLAWYQOK 60
 QY 61 PQQAPRLIYGASTRATGIDPRFSGSGSDFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 DB 61 PQQAPRLIYGASTRATGIDPRFSGSGSDFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 QY 121 QGTRLEIKGTVAAPSVFIFFPS 142
 DB 121 QGTRLEIKGTVAAPSVFIFFPS 142

RESULT 3
 AAY93702
 ID AAY93702 standard; protein; 235 AA.

XX AAY93702;
 AC AAY93702;

DT 03-OCT-2000 (first entry)

XX The kappa chain of immunoglobulin clone 4.1.1.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

PN WO200037504-A2.

PD 29-JUN-2000.

PF 23-DEC-1999; 99WO-US030895.

PR 23-DEC-1998; 98US-0113647P.

PA (PFIZ) PRIZER INC.

PA (ABGE-) AGENIX INC.

XX Hansen DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

DR WPI; 2000-442647/38.

DR N-PSDB; AAL46865.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

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PT treating, e.g. immune disorders.
XX
PS Claim 3; Fig 1A; 157pp; English.
XX
CC The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 235 AA;
    Query Match          93.0%; Score 682; DB 3; Length 235;
    Best Local Similarity 92.3%; Pred No. 1.2e-38;
    Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 METPAQLLLILLWLPDITGTEIATLQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLILLWLPDITGTEIATLQSPGTLSPGERATLSCRASQSFSSSYLAWYQOR 60
QY 61 PQAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCKYGTSAITFG 120
DB 61 PQAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCKYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIFPPS 142
DB 121 QGTRLEIKGTVAAPSVFIFPPS 142

RESULT 4
AAY93729
ID AAY93729 standard; protein; 235 AA.
XX
AC AAY93729;
XX
DT 03-OCT-2000 (first entry)
XX
DE The kappa chain of immunoglobulin clone 4.1.1.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
XX
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US030895.
XX
XX 23-DEC-1998; 98US-0113647P.
XX
XX (PFIZ ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX
XX WPI: 2000-442647/38.
XX N-PSDB; AAA46893.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

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PT -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX
PS Claim 3; Fig 22g; 157pp; English.
XX
CC The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 235 AA;
    Query Match          93.0%; Score 682; DB 3; Length 235;
    Best Local Similarity 92.3%; Pred No. 1.2e-38;
    Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 METPAQLLLILLWLPDITGTEIATLQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLLILLWLPDITGTEIATLQSPGTLSPGERATLSCRASQSFSSSYLAWYQOR 60
QY 61 PQAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCKYGTSAITFG 120
DB 61 PQAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCKYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIFPPS 142
DB 121 QGTRLEIKGTVAAPSVFIFPPS 142

RESULT 5
AAE35884
ID AAE35884 standard; protein; 235 AA.
XX
AC AAE35884;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human 4.1.1 anti-CTLA-4 antibody kappa chain.
XX
KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Protein 21..235
FT /note= "Mature anti-CTLA-4 antibody kappa chain"
XX
XX EP1262193-A1.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253652.
XX
XX 23-MAY-2001; 2001US-0293042P.
XX
XX (PFIZ ) PFIZER PROD INC.
XX
XX Hanson DC, Mueller EE;
XX
XX WPI: 2003-131215/13.
XX N-PSDB; AAD54344.
XX
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the

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PT preparation of medicament for the treatment of cancer.
XX
PS Disclosure; Fig 1G; 76pp; English.
XX
CC The invention relates to the use of human anti-cytotoxic T lymphocyte
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC cancer, cancer of the anal region, stomach cancer, breast cancer, cancer
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC The present sequence is human anti-CTLA-4 antibody kappa chain
XX
SQ Sequence 235 AA;
Query Match 93.0%; Score 682; DB 6; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.2e-38;
Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 METPAQLLFLLWLPTTGGTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
DB 1 METPAQLLFLLWLPTTGGTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIPTPPS 142
DB 121 QGTRLEIKGTVAAPSVFIPTPPS 142
RESULT 6
ABP71366
ID ABP71366 standard; protein; 235 AA.
XX
AC ABP71366;
XX
DT 28-APR-2003 (first entry)
XX
DE Anti-OPGL-1 antibody kappa light chain.
XX
KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
KW antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Region /note="IgG2 signal peptide"
FT Region 21..128
FT Region /note="variable region"
FT Region 129..235
FT Region /note="constant region"
XX
WO2003002713-A2.
XX
PN
XX
PD 09-JAN-2003.
XX
PF 25-JUN-2002; 2002WO-USO20181.
XX
PR 26-JUN-2001; 2001US-0301172P.
XX
PA (ABGE-) ABGENIX INC.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;
XX
WPI; 2003-210262/20.
XX
N-PSDB; ABZ59148.
XX
PT New antibodies that interact with osteoprotegerin ligands, useful for
PT treating osteoporosis disorders, e.g. osteoporosis, bone loss from
PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and

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PT osteonecrosis.
XX
PS Claim 1; Fig 4; 144pp; English.
XX
CC The invention relates to antibodies that interact with osteoprotegerin
CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
CC a biological sample. The antibody, or the pharmaceutical composition
CC comprising the antibody, is also useful for treating osteopenic disorder,
CC an inflammatory condition with attendant bone loss, an autoimmune
CC condition with attendant bone loss in a patient or rheumatoid arthritis
CC in a patient. In particular, the antibody or composition is useful for
CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'
CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
CC kappa light chain
XX
SQ Sequence 235 AA;
Query Match 90.9%; Score 666; DB 6; Length 235;
Best Local Similarity 90.1%; Pred. No. 1.5e-37;
Matches 128; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 METPAQLLFLLWLPTTGGTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
DB 1 METPAQLLFLLWLPTTGGTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIPTPPS 142
DB 121 QGTRLEIKGTVAAPSVFIPTPPS 142
RESULT 7
ADE28481
ID ADE28481 standard; protein; 234 AA.
XX
AC ADE28481;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 24-2-1 full length light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX
OS Homo sapiens.
XX
WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-USO36107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
WPI; 2003-441521/41.
XX
N-PSDB; ADE28480.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or

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PT viral infections.
XX
PS Claim 7; SEQ ID NO 88; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neurogenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody full length light chain protein of the invention.
XX
SQ Sequence 234 AA;

Query Match      89.8%; Score 658.5; DB 7; Length 234;
Best Local Similarity 90.1%; Pred. No. 4.7e-37;
Matches 128; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGIEALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGIEIVLTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
QY 61 PQQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120
DB 61 PQQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQY-SSLTFEG 119
QY 121 QGTRLEIKGTVAAPSVFIPTPPS 142
DB 120 PGTKVDIKRTVAAPSVFIPTPPS 141

RESULT 8
AAU74299
ID AAU74299 standard; protein; 236 AA.
XX
AC AAU74299;
XX
XX 12-MAR-2002 (first entry)
XX
DE Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
XX
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation;
KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX
OS Homo sapiens.
XX
XX WO200187981-A2.
XX
XX 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-JP004035.
XX
PR 18-MAY-2000; 2000JP-00147116.
XX
PR 30-MAR-2001; 2001JP-00099508.
XX
PA (NISE) JAPAN TOBACCO INC.
XX
FI Tsuji T, Teruka K, Hori N;
XX
XX WPI; 2002-075313/10.
XX
DR N-PSDB; AAS99475.
XX
```

```
XX New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
PS Claim 30; Page 284-285; 300pp; English.
XX
CC The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AILIM, for modulating proliferation
CC of AILIM-expressing cells, for modulating production of a cytokine from
CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
CC AILIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AILIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
CC AILIM monoclonal antibody amino acid sequences of the invention
XX
SQ Sequence 236 AA;

Query Match      89.8%; Score 658.5; DB 5; Length 236;
Best Local Similarity 89.5%; Pred. No. 4.7e-37;
Matches 128; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGIEALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGIEIVLTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
QY 61 PQQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAIT-TF 119
DB 61 PQQAPGLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQGFSSPMCSF 120
QY 120 QGTRLEIKGTVAAPSVFIPTPPS 142
DB 121 CQGTKLEIKRTVAAPSVFIPTPPS 143

RESULT 9
AAB47061
ID AAB47061 standard; protein; 143 AA.
XX
AC AAB47061;
XX
XX 08-MAY-2001 (first entry)
XX
XX Light chain variable region VL of KR1X1.
XX
KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;
KW complementarity determining region; CDR; MAb; B02C11.
KW conformational epitope; factor VIII; KR1X1; von Willebrand factor;
KW hemostasis; intravascular coagulation; arterial thrombosis;
XX
XX arterial restenosis; venous thrombosis; arteriosclerosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 43..54
XX FT /label= CDR1
XX FT Domain 69..75
XX FT /label= CDR2
XX
```

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FT Domain 109..118
FT /label= CDR3
XX
XX W0200104269-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-EP006677.
XX
XX 14-JUL-1999; 99GB-00016450.
XX
XX 14-JUL-1999; 99US-0143891P.
XX
XX (LEUV-) LEUVEN RES & DEV VZW.
XX
XX Jacquemin MG, Saint-Remy JR;
XX
XX WPI; 2001-138333/14.
XX
XX N-PSDB; AACB5454.
XX
XX Novel cell lines for producing monoclonal antibodies that bind to a
XX factor involved in hemostasis and coagulation cascade, useful for
XX treating and preventing coagulation disorders.
XX
XX Example 5; Fig 9; 55pp; English.
XX
XX This sequence represents the light chain variable region of the
XX monoclonal antibody (WAB), KR1X1. This MAB produced by the cell line of
XX the invention, specifically recognises the wild type factor VIII light
XX chain. KR1X1 can be used to inhibit the binding of factor VIII to von
XX Willebrand factor in a dose dependant manner. The new cell line KR1X 1.
XX is deposited with the Belgian Coordinated Collections of Micro-organisms,
XX under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally
XX with a thrombolytic agent, are useful for the treatment and/or prevention
XX of hemostasis, coagulation disorder or thrombotic pathologic condition
XX such as intravascular coagulation, arterial thrombosis, arterial
XX restenosis, venous thrombosis or arteriosclerosis, and attenuation of
XX coagulation in a mammal. An effective and safe antithrombotic therapy is
XX provided which reduces the risk of bleeding in mammals, more particularly
XX in humans
XX
XX Query Match 89.3%; Score 654.5; DB 4; Length 143;
XX Best Local Similarity 89.5%; Pred. No. 5.7e-37;
XX Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
XX
XX Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
XX Db 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
XX
XX Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFPAVYCYQKGTSA-ITF 119
XX Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFPAVYCYQKGTSA-ITF 119
XX
XX Qy 120 GQGTRLEIKGTVAAPSVFIPEPPS 142
XX Db 121 GGGTKVEIKRTVAAPSVFIPEPPS 143
XX
XX RESULT 10
XX AAC18879
XX ID AAC18879 standard; protein; 143 AA.
XX
XX AC AAC18879;
XX
XX XX 07-NOV-2002 (first entry)
XX
XX Human KR1X1 light chain variable region.
XX
XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
XX variable region; factor VIII inhibitor; sepsis; septic shock;
XX thrombus formation; systemic inflammatory response syndrome; CDR;
XX disseminated intravascular coagulation; haemophilia A; immunosuppressive;
XX

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KW complementarity determining region; antibacterial; antiinflammatory.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 43..54
XX /label= CDR1
XX Region 69..75
XX /label= CDR2
XX Region 108..117
XX /label= CDR3
XX
XX EP1222929-A2.
XX
XX 17-JUL-2002.
XX
XX 11-JAN-2002; 2002EP-00447005.
XX
XX 11-JAN-2001; 2001US-0261405P.
XX
XX (COLL-) COLLEN RES FOUND VZW D.
XX
XX Jacquemin MG, Saint-Remy JR;
XX
XX WPI; 2002-610270/66.
XX
XX N-PSDB; AAL49257.
XX
XX Pharmaceutical composition for treating systemic inflammatory response
XX syndrome, sepsis, septic shock and/or thrombus formation in
XX microvasculature in mammals, comprises a partial inhibitor of factor
XX VIII.
XX
XX Disclosure; Fig 13; 41pp; English.
XX
XX The present invention relates to a pharmaceutical composition for the
XX prevention and/or treatment of systemic inflammatory response syndrome
XX (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
XX and disseminated intravascular coagulation in mammals, comprising as an
XX active ingredient a partial inhibitor of factor VIII, in admixture with a
XX carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
XX present sequence is the light chain variable region of KR1X1
XX
XX Query Match 89.3%; Score 654.5; DB 5; Length 143;
XX Best Local Similarity 89.5%; Pred. No. 5.7e-37;
XX Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
XX
XX Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
XX Db 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
XX
XX Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFPAVYCYQKGTSA-ITF 119
XX Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFPAVYCYQKGTSA-ITF 119
XX
XX Qy 120 GQGTRLEIKGTVAAPSVFIPEPPS 142
XX Db 121 GGGTKVEIKRTVAAPSVFIPEPPS 143
XX
XX RESULT 11
XX AAY93704
XX ID AAY93704 standard; protein; 233 AA.
XX
XX AC AAY93704;
XX
XX XX 03-OCT-2000 (first entry)
XX
XX The kappa chain of immunoglobulin clone 4.8.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX

```


KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

OS WO200037504-A2.

PN 29-JUN-2000.

PD 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46867.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.

XX Claim 3; Fig 1B; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders

XX Sequence 233 AA;

Query Match 89.2%; Score 654; DB 3; Length 233;

Best Local Similarity 90.1%; Pred. No. 9.4e-37; Mismatches 4; Indels 2; Gaps 1;

Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDTTGTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

Db 1 METPAQLLFLLLWLPDTTGTGEIALTQSPGTLSPGERATLSGRATLSCRT--SVSSSYLAWYQOK 58

QY 61 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 120

Db 59 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 118

QY 121 QGTRLEIKGTVAAPSVFIFPPS 142

Db 119 GGTKVEIKRTVAAPSVFIFPPS 140

RESULT 12

AA93731

ID AA93731 standard; protein; 233 AA.

XX AA93731;

AC AA93731;

XX 03-OCT-2000 (first entry)

DT The kappa chain of immunoglobulin clone 4.8.1.

DE Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

XX proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

OS

XX Key Location/Qualifiers
FH 1.20
FT Peptide
/note= "signal peptide"

XX WO200037504-A2.

PN 29-JUN-2000.

PD 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46895.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.

XX Claim 3; Fig 22k; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders

XX Sequence 233 AA;

Query Match 89.2%; Score 654; DB 3; Length 233;

Best Local Similarity 90.1%; Pred. No. 9.4e-37; Mismatches 4; Indels 2; Gaps 1;

Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDTTGTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60

Db 1 METPAQLLFLLLWLPDTTGTGEIALTQSPGTLSPGERATLSCRT--SVSSSYLAWYQOK 58

QY 61 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 120

Db 59 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 118

QY 121 QGTRLEIKGTVAAPSVFIFPPS 142

Db 119 GGTKVEIKRTVAAPSVFIFPPS 140

RESULT 13

AAE35886

ID AAE35886 standard; protein; 233 AA.

XX AAE35886;

XX 17-JUN-2003 (first entry)

DT Human 4.8.1 anti-CTLA-4 antibody kappa chain.

DE Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;

XX cancer.

XX Homo sapiens.

OS

XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT /label= signal_peptide
XX FT Protein 21..233
XX FT /note= "Mature anti-CTLA-4 antibody kappa chain"
XX PN EP1262193-A1.
XX PD 04-DEC-2002.
XX PF 23-MAY-2002; 2002EP-00253652.
XX PR 23-MAY-2001; 2001US-0293042P.
XX PA (PFIZ) PFIZER PROD INC.
XX PI Hanson DC, Mueller EE;
XX DR WPI; 2003-131215/13.
XX DR N-PSDB; AAD54346.
XX PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
XX FT preparation of medicament for the treatment of cancer.
XX PS Disclosure; Fig 1K; 76pp; English.
XX CC The invention relates to the use of human anti-cytotoxic T lymphocyte
XX CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
XX CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
XX CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
XX CC cancer, cancer of the anal region, stomach cancer, breast cancer,
XX CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
XX CC The present sequence is human anti-CTLA-4 antibody kappa chain
XX SQ Sequence 233 AA;
Query Match 89.2%; Score 654; DB 6; Length 233;
Best Local Similarity 90.1%; Pred. No. 9.4e-37;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
QY 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSRCATLSRT--SVSSSYLAWYQQK 58
QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKYGTSATFG 120
DB 59 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKYGTSATFG 118
QY 121 QGTRLEIKGTVAAPSVFIPTPS 142
DB 119 GGTKEIKRTVAAPSVFIPTPS 140
RESULT 14
AAU74301 standard; protein; 236 AA.
XX AC AAU74301;
XX DT 12-MAR-2002 (first entry)
XX DE Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
XX KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
XX KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
XX KW immunosuppressive; dermatological; antinflammatory; hepatotropic;
XX KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
XX KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
XX KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
XX KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
XX KW systemic lupus erythematosus; autoimmune disorder; inflammation;
XX KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX OS Homo sapiens.
XX FN WO200187981-A2.
XX PD 22-NOV-2001.
XX PF 15-MAY-2001; 2001WO-JP004035.
XX PR 18-MAY-2000; 2000JP-00147116.
XX PR 30-MAR-2001; 2001JP-00099508.
XX PA (NISR) JAPAN TOBACCO INC.
XX PI Tsuji T, Tezuka K, Hori N;
XX DR WPI; 2002-075313/10.
XX DR N-PSDB; AAS99477.
XX CC New human monoclonal antibody that binds to activation inducible
XX CC lymphocyte immunomodulatory molecule, useful for treating rheumatoid
XX CC arthritis, multiple sclerosis and inflammation.
XX PS Claim 30; Page 298-299; 300pp; English.
XX CC The invention relates to a novel human antibody (I), preferably a human
XX CC monoclonal antibody which binds to an activation inducible lymphocyte
XX CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
XX CC transduction into a cell mediated by AILIM, for modulating proliferation
XX CC of AILIM-expressing cells, for modulating production of a cytokine from
XX CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
XX CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
XX CC AILIM-expressing cells. (I) is useful for treating, preventing or
XX CC prophylaxis of delayed type allergy. (I) is useful for treating and
XX CC preventing various diseases associated with AILIM-mediated costimulatory
XX CC transduction, and for inhibiting the onset and/or advancement of the
XX CC diseases. (I) is useful for suppression, prevention and/or treatment of
XX CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
XX CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
XX CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
XX CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
XX CC host reaction, graft versus host disease, immune rejection, disorders
XX CC caused by abnormal intestinal immunity, specifically inflammatory
XX CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
XX CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
XX CC immunorejection due to antigenicity to human, i.e., human anti-mouse
XX CC antigenicity (HANA) in a host. AAU74296-AAU74301 represent anti-human
XX CC AILIM monoclonal antibody amino acid sequences of the invention
XX SQ Sequence 236 AA;
Query Match 89.2%; Score 653.5; DB 5; Length 236;
Best Local Similarity 89.5%; Pred. No. 1e-36;
Matches 128; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
QY 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKYGTSAT-TF 119
DB 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKYGTSAT-TF 119
QY 120 GQGTREIKGTVAAPSVFIPTPS 142
DB 121 GQGTREIKRTVAAPSVFIPTPS 143
RESULT 15
AAU93733 standard; protein; 234 AA.
XX ID AAU93733
XX XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 33.3976 Seconds
(without alignments)
1116.513 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 MTPAQLLELLLLWLPDTG.....TRLEIKGVAPSVFIFFPS 142

Scoring table: BLOSUM62
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Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	733	100.0	142	14	US-10-044-569B-4
2	682	93.0	235	14	US-10-153-382-7
3	666	90.9	235	12	US-10-180-648-4
4	658.5	89.8	236	9	US-09-859-053-34
5	654.5	89.3	143	14	US-10-044-569B-8
6	654	89.2	233	14	US-10-153-382-11
7	653.5	89.2	236	9	US-09-859-053-38
8	650.5	88.7	234	14	US-10-153-382-15
9	649	88.5	150	10	US-09-782-397-5
10	600.5	81.9	236	11	US-09-833-245-237
11	596	81.3	128	15	US-10-309-764-89
12	590.5	80.6	127	15	US-10-309-762-95
13	590	80.5	384	15	US-10-391-265-804
14	590	80.5	384	15	US-10-391-265-805
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16	590	80.5	384	15	US-10-291-265-807
17	589.5	80.4	234	10	US-09-848-832-4
18	589.5	80.4	234	14	US-10-225-108A-4
19	589.5	80.4	234	15	US-10-461-148-2
20	587.5	80.2	127	15	US-10-309-762-91
21	584.5	79.7	127	15	US-10-309-762-93
22	579	79.0	215	15	US-10-307-724-122
23	574	78.3	307	15	US-10-291-265-332
24	574	78.3	312	15	US-10-291-265-334
25	573.5	78.2	226	10	US-09-453-234-50
26	573.5	78.0	226	10	US-09-453-234-86
27	571.5	78.0	226	10	US-09-453-234-80
28	570.5	77.8	238	14	US-10-216-484-107
29	570.5	77.8	238	14	US-10-384-933-107
30	565	77.1	215	10	US-09-972-656-100
31	564.5	77.0	226	10	US-09-453-234-42
32	564.5	77.0	238	14	US-10-216-484-50
33	564.5	77.0	238	14	US-10-384-933-50
34	561.5	76.6	226	10	US-09-453-234-74
35	559	76.3	141	14	US-10-153-382-23
36	558.5	76.2	224	10	US-09-453-234-52
37	556.5	75.9	119	14	US-10-226-615-4
38	556.5	75.9	119	15	US-10-374-932-4
39	556.5	75.9	226	10	US-09-453-234-72
40	554.5	75.6	226	10	US-09-453-234-38
41	552.5	75.4	224	10	US-09-453-234-44
42	552.5	75.4	224	10	US-09-453-234-76
43	552.5	75.4	224	10	US-09-453-234-78
44	550.5	75.1	224	10	US-09-453-234-40
45	548.5	74.8	129	15	US-10-309-764-105

ALIGNMENTS

RESULT 1

US-10-044-569B-4
; Sequence 4, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)..(162)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (205)..(225)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (325)..(351)
; OTHER INFORMATION: complementary determining region number three
; US-10-044-569B-4

Query Match 100.0%; Score 733; DB 14; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTPTAQLLFLLLWLPPDTTGEIATLQSPGTTLSLSPGERATLSLSCAQSPSSSSVLAWYQOK	60
Db	1	MTPTAQLLFLLLWLPPDTTGEIATLQSPGTTLSLSPGERATLSLSCAQSPSSSSVLAWYQOK	60
Qy	61	PQQAPELLIYGASTATCIPRFGSGSGDFTLTISRLEPEDFVAVYCKYKGTSAITFG	120
Db	61	PQQAPELLIYGASTATCIPRFGSGSGDFTLTISRLEPEDFVAVYCKYKGTSAITFG	120
Qy	121	QGTRLEIKGTVAAPSVFIFFPPS	142
Db	121	QGTRLEIKGTVAAPSVFIFFPPS	142

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RESULT 2
US_10-153-382-7
; Sequence 7, Application US/10153382
; Publication NO. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US_10-153-382-7

```

RESULT 3
US-10-180-648-4
; Sequence 4, Application US/10180648
; Publication No. US20040033535A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPGL
; FILING REFERENCE: 06843.0049-000000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-4

Query Match	90.9%;	Score 666;	DB 12;	Length 235;
Best Local Similarity	90.1%;	Pred. No. 2.7e-49;		
Matches 128;	Conservative 6;	Mismatches 8;	Indels 0;	Gaps 0;
Qy	1	METPAQLLFLLIWLPLEDTTGEIATLQTSPTGLISLPGERATLSCRASQSSSSSYLANVQOK	60	
Db	1	METPAQLLFLLIWLPLEDTTGEIIVLTQSPGTLSPGERATLSCRASQSVGRVLANVQOK	60	
Qy	61	PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLLTISRLEPEDFAVYVQKYGTSATIFG	120	
Db	61	PGQAPRLIIYGASSTRATGIPDRFSGSGGTDFLLTISRLEPEDFAVYVQOYGSSPRTFG	120	
Qy	121	QGTREIKGTVAAPSVEIFPPPS	142	
Db	121	QGTKEIKGTVAAPSVEIFPPPS	142	

RESULT 4
 US-09-859-053-34
 ; Sequence 34, Application US/09859053
 ; Patent No. US20020102658A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsuji, Takashi
 ; APPLICANT: Tezuka, Katsunari
 ; APPLICANT: Hori No. US20020102658A1uaki
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 ; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
 ; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
 ; FILE REFERENCE: 06501-079001
 ; CURRENT APPLICATION NUMBER: US/09/859,053
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: JP 2001-99508
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: JP 2000-147116
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-859-053-34

RESULT 5
US-10-044-569B-8
US-10-044-569B-8
; Sequence 8, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Collien Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical
composition for preventing
inflammatory response syndrome
and/or treating systemic
inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B

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; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)..(162)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (205)..(225)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (325)..(354)
; OTHER INFORMATION: complementary determining region number three
; US-10-044-569B-8

Query Match      89.3%; Score 654.5; DB 14; Length 143;
Best Local Similarity 89.5%; Pred. No. 1.5e-48;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY      1  METPAQLFLLLMLPDDTTGEBIALTQSPGTLISLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB      1  METPAQLFLLLMLPDDTTGEBIVLTQPGTLISLSPGERATLSCRASQSVASAYLAWYQOK 60

QY      61  PGCAPELLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGTGSA-ITF 119
DB      61  PGCAPELLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQYGTGSAITTF 120

QY      120  GGTRLEIKGTVAAPSVFIPEPS 142
DB      121  GGGTKVEIKRTVAAPSVFIPEPS 143

RESULT 6
US-10-153-382-11
; Sequence 11, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-382-11

Query Match      89.2%; Score 654; DB 14; Length 233;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      1  METPAQLFLLLMLPDDTTGEBIALTQSPGTLISLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB      1  METPAQLFLLLMLPDDTTGEBIVLTQSPGTLISLSPGERATLSCRT--SVSSSYLAWYQOK 58

QY      61  PGCAPELLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGTGSAITTF 120
DB      59  PGCAPELLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGTGSAITTF 118

QY      121  GGTRLEIKGTVAAPSVFIPEPS 142

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Db 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCKYGTSAITFG 120
Db 60 PGQAPRLIYGVSSRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCKYGTSAITFG 119
QY 121 QGTRLEIKGTVAAPSVFIIPPPS 142
Db 120 PGTKVDIKRTVAAPSVFIIPPPS 141

RESULT 9
US-09-782-397-5
; Sequence 5, Application US/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradipt K.
; Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,124
; FILING DATE: 1997-05-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-782-397-5

Query Match 88.5%; Score 649; DB 10; Length 150;
Best Local Similarity 87.7%; Pred. No. 4.7e-48;
Matches 128; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
Db 5 MEQPAQLLLLLWLPDITGVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOK 64
QY 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCKYGTSAITFG 118
Db 65 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCKYGTSAITFG 124
QY 117 ITFGGTRLEIKGTVAAPSVFIIPPPS 142

Db 125 ITFGGTRLEIKGTVAAPSVFIIPPPS 150

RESULT 10
US-09-833-245-237
; Sequence 237, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 237
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237

Query Match 81.9%; Score 600.5; DB 11; Length 236;
Best Local Similarity 84.7%; Pred. No. 1.1e-43;
Matches 122; Conservative 3; Mismatches 16; Indels 3; Gaps 2;

QY 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
Db 1 MEXPAQLLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCKYGT--SAIT 118
Db 60 PGQAPRLIYXASXATGIPARFSGSGSGTDFTLTISRLEPEDFAVYQCKXWPPXYT 119
QY 119 FGQGTREIKGTVAAPSVFIIPPPS 142
Db 120 FCXGTGKVEIKRTVAAPSVFIIPPPS 143

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RESULT 11
US-10-309-764-89
; Sequence 89, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-764-89

Query Match      81.3%; Score 596; DB 15; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.4e-43;
Matches 114; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSVYLAAYQOK 60
Db 1 METPAQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSIISALAYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120

QY 121 QGTRLEIK 128
Db 121 GGTKEIK 128

Query Match      80.6%; Score 590.5; DB 15; Length 127;
Best Local Similarity 89.8%; Pred. No. 4e-43;
Matches 115; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSVYLAAYQOK 60
Db 1 MEAPQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSVSYLAAYQOK 60

RESULT 12
US-10-309-762-95
; Sequence 95, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-95

Query Match      80.6%; Score 590.5; DB 15; Length 127;
Best Local Similarity 89.8%; Pred. No. 4e-43;
Matches 115; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSVYLAAYQOK 60
Db 1 MEAPQLLLFWLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSVSYLAAYQOK 60

RESULT 13
US-10-291-265-804
; Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 05/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-804

Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIATLQSPGTLSPGERATLSCRASQSSSVYLAAYQOKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSSSVYLAAYQOKPGQAPRLIIYGASTRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFGGTLRLKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFGGTLRLKGTVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291

RESULT 14
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
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; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASSRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQKYGTSAITFGQGTGLEIKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQGSPTTFGQGTKVDIKETVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291
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RESULT 15
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806
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Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASSRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQKYGTSAITFGQGTGLEIKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQGSPTTFGQGTKVDIKETVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291
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Search completed: April 5, 2004, 13:59:13
Job time : 34.3976 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:36:42 ; Search time 12.7343 Seconds
(without alignments)
575.678 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLLLLLLMLPDTTG.....TRLEIKGTVAAPSVFIPPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5B COMB.pdp:*
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4: /cgn2_6/prodata/2/1aa/6B COMB.pdp:*
5: /cgn2_6/prodata/2/1aa/PCITUS COMB.pdp:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	93.0	235	4	US-09-472-087-14 Sequence 14, Appl
2	682	93.0	235	4	US-09-472-087-65 Sequence 65, Appl
3	684	89.2	233	4	US-09-472-087-15 Sequence 15, Appl
4	654	89.2	233	4	US-09-472-087-67 Sequence 67, Appl
5	650.5	88.7	234	4	US-09-472-087-17 Sequence 17, Appl
6	650.5	88.7	234	4	US-09-472-087-69 Sequence 69, Appl
7	649	88.5	150	3	US-08-862-124-5 Sequence 5, Appl
8	624.5	85.2	134	1	US-08-405-034-4 Sequence 4, Appl
9	602	82.1	129	2	US-08-480-774A-4 Sequence 183, App
10	574	78.3	116	1	US-08-053-131-183 Sequence 46, Appl
11	574	78.3	116	2	US-08-096-762-183 Sequence 183, App
12	574	78.3	116	3	US-09-042-353-46 Sequence 46, Appl
13	574	78.3	116	4	US-08-758-417A-311 Sequence 311, App
14	573.5	78.2	226	4	US-09-456-090A-50 Sequence 50, Appl
15	573.5	78.2	226	4	US-09-456-090A-86 Sequence 86, Appl
16	571.5	78.0	226	4	US-09-456-090A-80 Sequence 80, Appl
17	564.5	77.0	226	4	US-09-456-090A-42 Sequence 42, Appl
18	561.5	76.6	226	4	US-09-456-090A-74 Sequence 74, Appl
19	560.5	76.5	234	3	US-09-049-672A-6 Sequence 6, Appl
20	559	76.3	141	4	US-09-472-087-88 Sequence 88, Appl
21	558.5	76.2	224	4	US-09-456-090A-52 Sequence 52, Appl
22	556.5	75.9	226	4	US-09-456-090A-72 Sequence 72, Appl
23	554.5	75.6	226	4	US-09-456-090A-38 Sequence 38, Appl
24	552.5	75.4	224	4	US-09-456-090A-44 Sequence 44, Appl
25	552.5	75.4	224	4	US-09-456-090A-76 Sequence 76, Appl
26	552.5	75.4	224	4	US-09-456-090A-78 Sequence 78, Appl
27	550.5	75.1	224	4	US-09-456-090A-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-472-087-14

; Sequence 14, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PFI

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-472-087-14

Query Match 93.0%; Score 682; DB 4; Length 235;

Best Local Similarity 92.3%; Pred. No. 1,2e-54;

Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 METPAQLLLLLLMLPDTTGTEIALTQSPGTLSPGGERATLSGRASQSFSSSYLIATYQOK 60

Db 1 METPAQLLLLLLMLPDTTGTEIVLTQSPGTLSPGGERATLSGRASQSISSFLATYQOR 60

QY 61 PQGAPRLIIYGASPRATGIDPRFSGSGGDTFTLTISRLPEDFAVYCYCKYGTSAITFG 120

Db 61 PQGAPRLIIYGASPRATGIDPRFSGSGGDTFTLTISRLPEDFAVYCYCKYGTSAITFG 120

QY 121 QGTRLEIKGTVAAPSVFIPPPS 142

Db 121 QGTRLEIKGTVAAPSVFIPPPS 142

RESULT 2

US-09-472-087-65

; Sequence 65, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

```

; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      93.0%; Score 682; DB 4; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.2e-54;
Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOK 60
Db 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOR 60

Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCOQYGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCOQYGTSAITFG 120

Qy 121 QGTRLEIKGTVAAPSVFIFFPPS 142
Db 121 QGTRLEIKGTVAAPSVFIFFPPS 142

US-09-472-087-15
Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 3
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15

Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOK 60
Db 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRAT--SVSSSYLANWYQOK 58

Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCOQYGTSAITFG 120
Db 59 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCOQYGTSAITFG 118

Qy 121 QGTRLEIKGTVAAPSVFIFFPPS 142
Db 119 GGTKEIKRTVAAPSVFIFFPPS 140

US-09-472-087-17
Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 5
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-472-087-17

Query Match 88.7%; Score 650.5; DB 4; Length 234;
Best Local Similarity 89.4%; Pred. No. 8.6e-52;
Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 METPAQLLFLLLWLPDITGTEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDITGTEIALTQSPGTLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
DB 60 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 119
QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
DB 120 PGTKVDIKRTVAAPSVFIIPPS 141

RESULT 6

US-09-472-087-69
; Sequence 69, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEORREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-69

Query Match 88.7%; Score 650.5; DB 4; Length 234;
Best Local Similarity 89.4%; Pred. No. 8.6e-52;
Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 METPAQLLFLLLWLPDITGTEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDITGTEIALTQSPGTLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
DB 60 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 119
QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
DB 120 PGTKVDIKRTVAAPSVFIIPPS 141

RESULT 7

US-08-862-124-5
; Sequence 5, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-862-124-5

Query Match 88.5%; Score 649; DB 3; Length 150;
Best Local Similarity 87.7%; Pred. No. 7.1e-52;
Matches 128; Conservative 6; Mismatches 8; Indels 4; Gaps 1;
QY 1 METPAQLLFLLLWLPDITGTEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 5 MEFOAQLLFLLLWLPDITGDIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 64
QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 116
DB 65 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 124
QY 117 ITFGQTRLEIKGTVAAPSVFIIPPS 142
DB 125 ITFGGKRVLEIKRTVAAPSVFIIPPS 150

RESULT 8

US-08-405-034-4
; Sequence 4, Application US/08405034
; Patent No. 5744585
; Patent No. 5744585 5712371
; GENERAL INFORMATION:
; APPLICANT: Medenica, Rajko D.
; APPLICANT: Mukerjee, Sonjoy
; TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
; TITLE OF INVENTION: Carcinoma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,034
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34656.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-405-034-4

Query Match      85.2%; Score 624.5; DB 1; Length 134;
Best Local Similarity 91.8%; Pred. No. 1e-49;
Matches 123; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY      1  METPAQLLFLLLWLPTTTCIEALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB      1  METPAQLLFLLLWLPTTTCIEALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60

QY      61  PGQAPRLLYGASTRATGIPDRFSGSGSGDTFTLTISRLEPEDFAVYVCQKYGTS-ITF 119
DB      61  PGQAPSLIYGASTRATGIPDRFSGSGSGDTFTLTISRLEPEDFAVYVCQYGGSSARYTF 120

QY      120  GQGTRLLEIKGTVA 133
DB      121  GQGTKLEIKGTVA 134

RESULT 9
US-08-480-774A-4
Sequence 4, Application US/08480774A
Patent No. 5853186
GENERAL INFORMATION:
APPLICANT: MARASCO, Wayne A.
APPLICANT: SODROSKI, Joseph G.
APPLICANT: HASELTINE, William A.
APPLICANT: POSNER, Marshall R.
TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
TITLE OF INVENTION: ANTI-SP 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,774A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/400,674
FILING DATE: 08-MAR-1995
APPLICATION NUMBER: 07/804,652
FILING DATE: 10-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S

```

```
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-183

Query Match      78.3%; Score 574; DB 1; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 METPAQLFLLWLPTTGTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLWLPTTGTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 60
QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYQYKGS 115
DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYQYKGS 115

RESULT 11
US-08-096-762-183
; Sequence 183, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-183

Query Match      78.3%; Score 574; DB 2; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 METPAQLFLLWLPTTGTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLWLPTTGTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 60
QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYQYKGS 115
DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYQYKGS 115

RESULT 12
US-09-042-353-46
; Sequence 46, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-353-46

Query Match 78.3%; Score 574; DB 3; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60

Qy 61 PQAPRLIYGASTRATGIDPRFSGSGSGTDFLTISRLEPEDFAVYQCQYKTS 115
Db 61 PQAPRLIYGASTRATGIDPRFSGSGSGTDFLTISRLEPEDFAVYQCQYKTS 115

RESULT 13
US-08-758-417A-311
Sequence 311, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 311:
US-08-758-417A-311

Query Match 78.3%; Score 574; DB 4; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60

Qy 61 PQAPRLIYGASTRATGIDPRFSGSGSGTDFLTISRLEPEDFAVYQCQYKTS 115
Db 61 PQAPRLIYGASTRATGIDPRFSGSGSGTDFLTISRLEPEDFAVYQCQYKTS 115

RESULT 14
US-09-456-090A-50
Sequence 50, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 50
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 78.2%; Score 573.5; DB 4; Length 226;
Best Local Similarity 91.9%; Pred. No. 8.2e-45;
Matches 113; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 60
QY 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVFIF 139
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVFIF 120
QY 140 PPS 142
DB 121 PPS 123

RESULT 15
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buécher, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 78.2%; Score 573.5; DB 4; Length 226;
Best Local Similarity 91.9%; Pred. No. 8.2e-45;
Matches 113; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 60
QY 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVFIF 139
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVFIF 120
QY 140 PPS 142
DB 121 PPS 123

Search completed: April 5, 2004, 13:44:08
Job time : 12.7343 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 12.6701 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-6

Perfect score: 837

Sequence: 1 MDWTWRILFLVAATGAHSQ.....GVTSHYFDYWGRTLVTVSS 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR 78:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	606.5	72.5	135	2 S49530	anti-Sm antibody V
2	591.5	70.7	171	2 S23623	Ig heavy chain V r
3	550	65.7	117	2 S18551	Ig heavy chain V r
4	549.5	65.7	136	2 S31600	Ig heavy chain V r
5	548	65.5	117	1 HVHU035	Ig heavy chain pre
6	540	64.5	117	2 S31680	Ig heavy chain V r
7	523.5	62.5	132	2 S31596	Ig heavy chain V r
8	521	62.2	160	2 PLO105	anti-PR2 erythrocy
9	517	61.8	148	2 S29257	Ig heavy chain V r
10	515	61.5	142	2 S19245	Ig heavy chain pre
11	505	60.3	129	2 S46393	Ig heavy chain V r
12	502	60.0	123	2 D33548	Ig heavy chain V-1
13	498	59.5	142	2 A32483	Ig heavy chain V r
14	493	58.9	117	2 S18553	Ig heavy chain V r
15	491	58.7	134	2 S21516	Ig heavy chain V r
16	490.5	58.6	118	2 S36265	Ig heavy chain V r
17	489	58.4	627	2 S14683	Ig mu chain precu
18	486	58.1	117	1 HVHUHG	Ig heavy chain pre
19	482.5	57.6	143	1 E1HUND	Ig heavy chain pre
20	477	57.0	117	2 S18554	Ig heavy chain V r
21	474	56.6	131	2 S21924	Ig heavy chain pre
22	465	55.6	117	2 PT0371	Ig gamma chain pre
23	464.5	55.5	139	1 MHMS18	Ig heavy chain pre
24	462.5	55.3	137	2 C41287	Ig heavy chain V r
25	460	55.0	117	2 S18554	Ig heavy chain pre
26	456	54.5	138	1 HVMS7	Ig heavy chain pre
27	454	54.2	104	2 S69899	Ig heavy chain V r
28	453.5	54.2	110	2 PH1669	Ig heavy chain V r
29	450.5	53.8	135	2 A30577	Ig heavy chain pre

30 450 53.8 138 2 E32513 Ig heavy chain pre
31 447 53.4 111 2 S21925 Ig heavy chain V r
32 446 53.3 98 2 S26938 Ig heavy chain V r
33 443 52.9 121 2 S20783 Ig heavy chain V r
34 439.5 52.5 137 1 G2MS43 Ig heavy chain pre
35 438.5 52.4 116 2 S31698 Ig heavy chain V r
36 438 52.3 98 2 S26912 Ig heavy chain V r
37 438 52.3 109 2 PH1668 Ig heavy chain pre
38 437.5 52.3 137 2 F29380 Ig gamma-2b chain
39 437.5 52.3 474 1 G2MS11 Ig heavy chain V r
40 436.5 52.2 116 2 S31667 Ig heavy chain pre
41 435.5 52.0 137 2 H32513 Ig heavy chain V r
42 435 52.0 127 2 S34014 Ig heavy chain V r
43 434 51.9 126 2 I44151 Ig heavy chain V r
44 433.5 51.8 137 2 E29380 Ig heavy chain pre
45 433.5 51.8 469 2 S37483 Ig gamma-2a chain

ALIGNMENTS

RESULT 1

S49530

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C:Species: Homo sapiens (man)

C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

C:Accession: S49530

R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797

A:Accession: S49530

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <MAH>

A:Cross-references: EMBL:Z46348; NID:9560839; PIDN:CAA86467.1; PID:9560840

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMW>

Query Match 72.5%; Score 606.5; DB 2; Length 135;

Best Local Similarity 77.6%; Pred. No. 4.9e-46;

Matches 121; Conservative 6; Mismatches 8; Indels 21; Gaps 3;

QY 1 MDWTWRILFLVAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTQYSASGHFTA 60

Db 1 MDWTWRILFLVAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVQAPQGGLEWNGRINPNSGATDYAHKFGQRTVMSRDTISISTAYNELSLTSDDT 120

Db 51 YVHWVQAPQGGLEWNGRINPNSGGTNYAQKFGRTVTRDTISISTAYNELSLRSDDT 110

QY 121 AMYTCARADNYFDIVTGTVTSHTSYFDYWGRTLVTVSS 156

Db 111 AVYTCARAR-----TGY-----NYWQGGLTVTVSS 135

RESULT 2

S23623

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23623

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-171 <OLE>

A:Cross-references: EMBL:X59702; NID:932010; PIDN:CAA42223.1; PID:932011

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 591.5; DB 2; Length 171;
Best Local Similarity 75.0%; Pred. No. 1.3e-44;
Matches 117; Conservative 9; Mismatches 19; Indels 11; Gaps 2;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDDT 120
DB 51 YQHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDDT 110
QY 121 AMYICARADNFDIVTGYTSHYFDYWGRTLVTVSS 156
DB 111 AVYICARADNFDIVTGYTSHYFDYWGRTLVTVSS 145

RESULT 3

S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SH>
A:Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
J:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Defos, M.; Kozin, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 550; DB 2; Length 117;
Best Local Similarity 83.5%; Pred. No. 3.6e-41;
Matches 106; Conservative 4; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDDT 120
DB 51 YQHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDDT 110
QY 121 AMYICAR 127
DB 111 AVYICAR 117

RESULT 4

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CU>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 549.5; DB 2; Length 136;
Best Local Similarity 69.9%; Pred. No. 4.7e-41;
Matches 109; Conservative 12; Mismatches 14; Indels 21; Gaps 2;
QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDDT 120
DB 51 YDINWVRQATGQGLEWMGRINPNSGATGYAKFGQGRVTMTNTSISTAYMELSLRSDT 110
QY 121 AMYICARADNFDIVTGYTSHYFDYWGRTLVTVSS 156
DB 111 AVYICARWDAFDI-----WGQIMTVTVSS 135

RESULT 5

HVHU35
Ig heavy chain precursor V region (V35) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S00476; S34013
R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh
EMBO J. 7, 1047-1051, 1988
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain 1
A:Reference number: S00476; MUID:88296408; PMID:2841108
A:Accession: S00476
A:Molecule type: DNA
A:Residues: 1-117 <MATS>
A:Cross-references: EMBL:X07448; NID:g33104; PIDN:CA856703.1; PID:g6002173
A:Note: The authors translated the codon AGT for residue 89 as Met
R:Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34013
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 20-116 <MAR>
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 548; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 5.4e-41;
Matches 105; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDT 120

Db 51 YMHVVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 110

Qy 121 AMYYCAR 127

Db 111 VVYYCAR 117

RESULT 6

S31680

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31680

R:Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31680

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <CUI>

A:Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796

C:Genetics: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 540; DB 2; Length 117;

Best Local Similarity 81.1%; Pred. No. 2.7e-40;

Matches 103; Conservative 7; Mismatches 7; Indels 10; Gaps 1;

Qy 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Qy 61 YSVHWVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 120

Db 51 YMHVVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 110

Qy 121 AMYYCAR 127

Db 111 VVYYCAR 117

RESULT 7

S31596

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31596

R:Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31596

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <CUI>

A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 523.5; DB 2; Length 132;

Best Local Similarity 67.3%; Pred. No. 8.4e-39;

Matches 105; Conservative 11; Mismatches 15; Indels 25; Gaps 2;

Qy 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Qy 61 YSVHWVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 120

Db 51 YDIDWVRQATGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRABDT 110

Qy 121 AMYYCARADNYFDIVTGYTSHYFDYGRGTLTVSS 156

Db 111 AVYYLAKA-----PAWGQGTMTVTVSS 131

RESULT 8

PL0105

anti-Pr2 erythrocyte autoantibody heavy chain precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996

C:Accession: PL0105

R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec

A:Reference number: PL0106; MUID:89235583; PMID:2541221

A:Accession: PL0105

A:Molecule type: mRNA

A:Residues: 1-160 <SIL>

A>Note: the authors translated the codon GAC for residues 108 and 109 as Glu

C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blc

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: autoantibody; hemagglutinin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:34-117/Domain: immunoglobulin homology <IMM>

F:49-54/Region: complementarity-determining 1

F:69-84/Region: complementarity-determining 2

F:118-131/Domain: D region <DRG>

F:132-144/Domain: J4 segment <JSG>

F:145-160/Domain: C region <CRG>

Query Match 62.2%; Score 521; DB 2; Length 160;

Best Local Similarity 67.9%; Pred. No. 1.7e-38;

Matches 106; Conservative 8; Mismatches 30; Indels 12; Gaps 2;

Qy 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Qy 61 YSVHWVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 120

Db 51 YGISWVRQAPGQGLEWGMGRINPNSGGTNYAQKFGQRTVTSRTDTSISTAYMELSLRSDDT 110

Qy 121 AMYYCARADNYFDIVTGYTSHYFDYGRGTLTVSS 156

Db 111 AVYYCARAPGYCSGGGCTRGD--DYWGQGLTVTVSS 144

RESULT 9

S29257

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S29257

R:Chouchane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.

Eur. J. Biochem. 207, 1115-1121, 1992

A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment

A:Reference number: S29257; MUID:92362614; PMID:1499555

A:Accession: S29257

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <CHO>

A:Cross-references: GB:S42403; NID:g253699; PIDN:AA22940.1; PID:g253700

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 517; DB 2; Length 148;

Best Local Similarity 65.4%; Pred. No. 3.5e-36;

Matches 104; Conservative 15; Mismatches 26; Indels 14; Gaps 3;

Qy 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYT-----PAM 50
Qy 61 YSVHWVRQAPGQGLEWGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTT 120
Db 51 YALHWVRQAPGQGLEWGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTT 110
Qy 121 AMYICARADNYFDIVTGY---TSHYFDYWGRTLVTVSS 156
Db 111 AVTYCARSPR-INMVRGLITTPPPWFDMSWGQGLTVTVSS 148

RESULT 10

Ig heavy chain precursor V region (10P1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S19245
R:Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
EMBO J. 11, 603-609, 1992
A:Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A:Reference number: S19245; MUID:92164649; PMID:1537339
A:Accession: S19245
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-142 <KIR>
A:Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 61.5%; Score 515; DB 2; Length 142;
Best Local Similarity 64.7%; Pred. No. 5e-38;
Matches 101; Conservative 20; Mismatches 21; Indels 14; Gaps 3;

Qy 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYT-----FTS 60
Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYT-----FTS 50
Qy 61 YSVHWVRQAPGQGLEWGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTT 120
Db 51 YANWVRQAPGQGLEWGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTT 110
Qy 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 111 AVTYCARA--YTLWMTAVT--HFDWVGQGLTVTVSS 142

RESULT 11

Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FTG>
A:Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 505; DB 2; Length 129;
Best Local Similarity 72.7%; Pred. No. 3.4e-37;
Matches 101; Conservative 8; Mismatches 18; Indels 12; Gaps 2;
Qy 20 QVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVRQAPGQGLEWGR 79

Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTG-----YMHVWRQAPGQGLEWGR 50
Qy 80 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTTAMYYCARADNYFDIVTGYT 139
Db 51 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTTAVYYCARDASYYVDSSGY 110
Qy 140 S--HYFDYWGRTLVTVSS 156
Db 111 SANYYMDVWGKGTITVTVSS 129

RESULT 12

Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.0%; Score 502; DB 2; Length 123;
Best Local Similarity 72.5%; Pred. No. 5.9e-37;
Matches 100; Conservative 10; Mismatches 12; Indels 16; Gaps 3;

Qy 20 QVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVRQAPGQGLEWGR 79
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTG-----YMHVWRQAPGQGLEWGR 50
Qy 80 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTTAMYYCARADNYFDIVTGYT 139
Db 51 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTTAVYYCARAS-----YCGYD 105
Qy 140 SHY--FDYWGRTLVTVSS 156
Db 106 CYFFDYWGQGLTVTVSS 123

RESULT 13

Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
R:Larick, J.W.; Danielson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck,
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us
A:Reference number: A32483; MUID:89273586; PMID:2499327
A:Accession: A32483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 59.5%; Score 498; DB 2; Length 142;
Best Local Similarity 67.8%; Pred. No. 1.5e-36;
Matches 103; Conservative 10; Mismatches 19; Indels 20; Gaps 4;

Qy 10 LVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVRQA 69
Db 1 LLVAPGAHSQVQLVQSGAEVKKPGASVKVCKASGYTFTN-----YYMEVWRQA 50

```
QY 70 PQGLEWGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDTAMYYCAR-- 127
Db 51 PQGLEWGIINPSGNSINACKFGQRTVMTREDTSTSVYMELSLSLASEDTAVYYCAREK 110
QY 128 -ADNYFD--IVTGYTSHYFDYNGRGLTVTVSS 156
Db 111 LATTIFGVLIITG-----MDYWGQGLTVTVSS 137

RESULT 14
S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18553; S26916
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3643-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:932871; PIDN:CAA78197.1; PID:932872
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 493; DB 2; Length 117;
Best Local Similarity 74.8%; Pred. No. 3.4e-36;
Matches 95; Conservative 9; Mismatches 13; Indels 10; Gaps 1;

QY 1 MDWTWILFLVAATGAHSQVQLVQSGAEVKPGASVKVSCKTSQYNYFTGYSASGHIFTA 60
Db 1 MDWTWILFLVAATGVHSQVQLVQSGAEVKPGASVKVSCKASGYT-----FTS 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDT 120
Db 51 YAMHWVRQAPGQRLWNGWMINAGNGNTKYSQKFGQRTITRDTSTASTAYMELSLRLSEDT 110
QY 121 AMYYCAR 127
Db 111 AVYYCAR 117

RESULT 15
S21916
Ig heavy chain V region precursor - human (fragment)
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 21-Jan-2000
C:Accession: S21916
R:Mierau, R.; Gause, A.; Kueppers, R.; Michels, M.; Mageed, R.A.; Jefferis, R.; Genth, E
submitted to the EMBL Data Library, July 1991
A:Description: A Human monoclonal IgA rheumatoid factor using the Vk(IV) light chain gen
A:Reference number: S21916
A:Accession: S21916
A:Molecule type: mRNA
A:Residues: 1-134 <MIE>
A:Cross-references: EMBL:X61124; NID:933286; PIDN:CAA43436.1; PID:933287
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

```
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-134/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 491; DB 2; Length 134;
Best Local Similarity 59.6%; Pred. No. 5.9e-36;
Matches 93; Conservative 19; Mismatches 22; Indels 22; Gaps 2;

QY 1 MDWTWILFLVAATGAHSQVQLVQSGAEVKPGASVKVSCKTSQYNYFTGYSASGHIFTA 60
Db 1 MDWTWILFLVAATGAHSQVQLVQSGSELKPGASVKVSCKASGYTFN----- 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDT 120
Db 51 YALNWLRLQAPGQGLEWMGWINTNTGKTAQAFTGRFVFLSDTSVSTTYLIQISSLKRAEDT 110
QY 121 AMYYCARADNYFDIVTGYTSHYFDYNGRGLTVTVSS 156
Db 111 AVYFCAR-----DRWNDYWGQGTQVTVSS 134

Search completed: April 5, 2004, 13:43:02
Job time : 12.6701 secs
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QY 61 YSVHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 120
Db 51 YNHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 110
QY 121 AMYTCAR 127
Db 111 VVYTCAR 117

RESULT 2
HV1C HUMAN STANDARD; PRT; 147 AA.
AC P0174;
DT 21-JUL-1986 (Rel. 01, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR SVART; IPR003596; Ig_v.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin V region; Signal;
FT SIGNAL 1 19 IG HEAVY CHAIN V-I REGION ND.
FT CHAIN 20 147 IG-LIKE.
FT DOMAIN 20 131 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 20 20
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147
SQ SEQUENCE 147 AA; 16491 MW; 9489F72A5366C20 CRC64;

Query Match 58.5%; Score 489.5; DB 1; Length 147;
Best Local Similarity 60.6%; Pred. No. 6.5e-41;
Matches 97; Conservative 19; Mismatches 27; Indels 17; Gaps 4;

QY 1 MDWTRILFLVAATGAHSQVQLVSGAEVKKPKASVKVCKSGYNFTGYSGASGHIFTA 60
Db 1 MDWTRILFLVAATGAHSQVQLVSGAEVKKPKASVKVCKSGYNFTGYSGASGHIFTA 51
QY 61 YSVHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 120
Db 52 Y-IHWIRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 110
QY 121 AMYTCARAD----NYFDIVTGTYTHYFDYWGRLVTVSS 156
Db 121 AMYTCARAD----NYFDIVTGTYTHYFDYWGRLVTVSS 110
```

```
Db 111 AVFYCAKSDPFNSDYNFDSYTYT---LDVWGQGTITTVSS 147
RESULT 3
HV1B HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
DR HSSP; P01772; 2PBH4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V-I REGION HG3.
FT CHAIN 20 117 IG-LIKE.
FT DOMAIN 20 >117
FT NON_TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 58.1%; Score 486; DB 1; Length 117;
Best Local Similarity 72.4%; Pred. No. 1.1e-40;
Matches 92; Conservative 9; Mismatches 16; Indels 10; Gaps 1;

QY 1 MDWTRILFLVAATGAHSQVQLVSGAEVKKPKASVKVCKSGYNFTGYSGASGHIFTA 60
Db 1 MDWTRILFLVAATGAHSQVQLVSGAEVKKPKASVKVCKSGYNFTGYSGASGHIFTA 50
QY 61 YSVHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 120
Db 51 YNHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLRSDDT 110
QY 121 AMYTCAR 127
Db 111 AVYTCAR 117

RESULT 4
HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -
CC DR PIR; A90809; MHMS18.
CC DR PDB; 1A6U; 27-MAY-98.
CC DR PDB; 1A6W; 15-JUL-98.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_V.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS0835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal; 3D-structure.
CC KW SIGNAL 1 19 IG HEAVY CHAIN V REGION B1-8/186-2.
CC FT CHAIN 20 139
CC FT DOMAIN 20 49
CC FT DOMAIN 50 54
CC FT DOMAIN 55 68
CC FT DOMAIN 69 85
CC FT DOMAIN 86 117
CC FT DOMAIN 118 124
CC FT DOMAIN 125 139
CC FT DISULFID 41 143
CC FT NON_TER 139 139
CC SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

CC Query Match 55.5%; Score 464.5; DB 1; Length 139;
CC Best Local Similarity 57.7%; Pred. No. 1.7e-38;
CC Matches 90; Conservative 20; Mismatches 29; Indels 17; Gaps 2;

QY 1 MDWTWILFLVAATGAHQSVQLVQSGAEVKKPGASVKVSCKTSYNYFTGYSASGHIFTA 60
Db 1 MGSWCIIMFLAATATGVHSQVQLQPGAEIVKPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWVROAPGQGLEWGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRTSDDT 120
Db 51 YNHWVKQRPQGLEWIGRIDPNSGQTKNEKSKAILTVDPKPSITAYMQLSSLTSDS 110
QY 121 AMYICAPADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 111 AVYICARYDY-----YGSYFDYWGQGTTLTVSS 139

CC RESULT 5
CC HV48_MOUSE STANDARD; PRT; 138 AA.
CC AC P03980;
CC DT 23-OCT-1986 (Rel. 02, Created)
CC DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=84248078; PubMed=6429663;
RX Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgG-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
CC PIR; A02033; HVMST7.
CC DR HSP; P01810; 2FBJ.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_V.
CC DR Pfam; PF00047; ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS0835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW SIGNAL 1 20 IG HEAVY CHAIN V REGION TEPC 1017.
CC FT CHAIN 21 138
CC FT DOMAIN 21 49
CC FT DOMAIN 50 54
CC FT DOMAIN 55 68
CC FT DOMAIN 69 85
CC FT DOMAIN 86 117
CC FT DOMAIN 118 127
CC FT DOMAIN 128 138
CC FT DISULFID 41 115
CC FT NON_TER 138 138
CC SQ SEQUENCE 138 AA; 15576 MW; 748157F4C6907B8E CRC64;

CC Query Match 54.5%; Score 456; DB 1; Length 138;
CC Best Local Similarity 55.8%; Pred. No. 1.1e-37;
CC Matches 87; Conservative 23; Mismatches 28; Indels 18; Gaps 2;

QY 1 MDWTWILFLVAATGAHQSVQLVQSGAEVKKPGASVKVSCKTSYNYFTGYSASGHIFTA 60
Db 1 MGSWCIIMFLAATATGVHSQVQLQPGAEIVKPGASVKLSCK-----ASGHFTN 50
QY 61 YSVHWVROAPGQGLEWGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRTSDDT 120
Db 51 YNHWVKQRPQGLEWIGRIDPNSGQTKNEKSKAILTVDPKPSITAYMQLSSLTPEEF 110
QY 121 AMYICAPADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 111 AVYICARSDGYD-----WFWYWGQGTTLTVFSA 138

CC RESULT 6
CC HV11_MOUSE STANDARD; PRT; 137 AA.
CC AC P01755;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE IG heavy chain V region 843 precursor.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=81234548; PubMed=6788376;
CC RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
CC RA Baltimore D.;
CC RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
CC RL Cell 24:625-637(1981).
CC CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA


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CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPE ANTIBODIES).
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CC -----
DR EMBL; J00539; AAA38172.1; -
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 52.5%; Score 439.5; DB 1; Length 137;
Best Local Similarity 55.1%; Pred. No. 4.6e-36;
Matches 86; Conservative 18; Mismatches 33; Indels 19; Gaps 2;

QY 1 MDWTWILFLVAATAAGAHQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MGWSCIMFLAATATGVHSEVQLQPGAEFVPPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWYRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDT 120
DB 51 YLMHWYNQRPGRGLEWIGRIDPNSGGTTNEHFRSKATLTIDKPSSTAYMQLSLTSDS 110
QY 121 AMYTCARADNYFDIVGTYSHPYDYGWGRGLTVSS 156
DB 111 AVYTCARY-----RLGRYDYGWQGTTLTVSS 137

RESULT 7
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; J00493; AAA38128.1; -
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 49.7%; Score 416; DB 1; Length 140;
Best Local Similarity 50.6%; Pred. No. 9.3e-34;
Matches 79; Conservative 29; Mismatches 32; Indels 16; Gaps 2;

QY 1 MDWTWILFLVAATAAGAHQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MGWSCIFLFLSVTAGVHSEVQLQPGAEVLRAGSSVKMSCKASGYT-----FTS 50
QY 61 YSVHWYRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDT 120
DB 51 YGNWVKQRPQGLEWIGVINPQNGVINYNEKFGKGTTLTVDKSSSTAYMQLSLTSDS 110
QY 121 AMYTCARADNYFDIVGTYSHPYDYGWGRGLTVSS 156
DB 111 AVYFCARSHYYG-----SYDEYDYGWQGTTLTVSS 140

RESULT 8
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; J00494; AAA38130.1; -
DR PIR; A02042; HVMSB1.
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Query Match 48.0%; Score 402; DB 1; Length 117;

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[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RL Cell 40:271-281(1985).
CC -----
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CC -----
DR EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;
Query Match 45.5%; Score 381; DB 1; Length 117;
Best Local Similarity 56.7%; Pred. No. 2e-30;
Matches 72; Conservative 18; Mismatches 27; Indels 10; Gaps 1;
QY 1 MDWTWRIFLVAATGAHSOVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSGASGHIFTA 60
DB 1 MGNSCILFLAATATGVSHPVQLQPGAEVLKPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYNELSLRTSDDT 120
DB 51 YWHEWVKRQPGQGLEWIGRIHPSDSDTNYNQKPKGKATLTVDKPSSTAYMQLSSLTSEDS 110
QY 121 AMYICAR 127
DB 111 AVYICTR 117
RESULT 13
HV10 MOUSE
ID HV10 MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RX Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
DR PIR; A02032; HVM502.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
Query Match 47.3%; Score 396; DB 1; Length 117;
Best Local Similarity 60.3%; Pred. No. 6.8e-32;
Matches 76; Conservative 17; Mismatches 23; Indels 10; Gaps 1;
QY 1 MDWTWRIFLVAATGAHSOVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSGASGHIFTA 60
DB 1 MGNSCILFLAATATGVSHPVQLQPGAEVLKPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYNELSLRTSDDT 120
DB 51 YWHEWVKRQPGQGLEWIGRIHPSDSDTNYNQKPKGKATLTVDKSSSTAYMQLSSLTSEDS 110
QY 121 AMYICA 126
DB 111 AVYICA 116
RESULT 12
HV49 MOUSE
ID HV49 MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region VH558 B4 precursor.
GN Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24-625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00533; AAA38602.1; -.
CC DR PIR; C90809; HVMS45.
CC DR HSSP; P01810; 2FBJ.
CC DR MGD; MGI:96486; Igh-VJ558.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 19
CC FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT NON_TER 117 117
CC SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 45.4%; Score 380; DB 1; Length 117;
Best Local Similarity 57.5%; Pred. No. 2.5e-30;
Matches 73; Conservative 18; Mismatches 26; Indels 10; Gaps 1;

QY 1 MDWTWILFLVAAATGAHQVQLVQSGAEVKVPGASVKYCKTSQYNFTGYSGASGHIFTA 60
Db 1 MGWSCIMFLAATATGVHFQVQLQPGAEIVKPGASVKLSKASGYT-----FTS 50

QY 61 YSVHWYRQAPGQLEWNGINPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSTSDT 120
Db 51 YNHWYKQRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTS 110

QY 121 AMYICAR 127
Db 111 AVYICAR 117

RESULT 14
HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Sekevitiz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiootype response of the strain 'A' mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J

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CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; LMCP.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC KW Immunoglobulin V region; Hybridoma.
CC FT DOMAIN 1 111 IG-LIKE.
CC FT NON_TER 120 120
CC SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 45.4%; Score 380; DB 1; Length 120;
Best Local Similarity 53.7%; Pred. No. 2.6e-30;
Matches 73; Conservative 23; Mismatches 24; Indels 16; Gaps 2;

QY 21 VQLVQSGAEVKVPGASVKYCKTSQYNFTGYSGASGHIFTAYSVHWYRQAPGQLEWNGRI 80
Db 1 VQLQCGAEIVKPGASVKYCKTSQYNFTGYSGASGHIFTAYSVHWYRQAPGQLEWNGRI 50

QY 81 NPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSTSDTAMYICARADNYFDIVTGYTS 140
Db 51 NPGNGYTKYNEKFKGKTLTVDKSSSTAYMQLSLTSSEDSAVYFCARSVYGG-----S 104

QY 141 HYPDYWGRCGLTVTVSS 156
Db 105 YYPDYWGCGTTLTVTVSS 120

RESULT 15
HV50 MOUSE STANDARD; PRT; 120 AA.
ID HV50 MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).
CC DR PIR; A02037; MHMS15.
CC DR HSSP; P01810; 2FBJ.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC KW Immunoglobulin V region.
CC FT DOMAIN 1 98 V SEGMENT.
CC FT DOMAIN 99 105 D SEGMENT.
CC FT DOMAIN 106 120 J SEGMENT.
CC FT DISULFID 22 96 BY SIMILARITY.
CC FT NON_TER 120 120
CC SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 44.6%; Score 373.5; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 1.1e-29;
Matches 73; Conservative 18; Mismatches 29; Indels 17; Gaps 2;

QY 20 VQLVQSGAEVKVPGASVKYCKTSQYNFTGYSGASGHIFTAYSVHWYRQAPGQLEWNGRI 79
Db 1 VQLQLQPGTEIVKPGASVNLKSKASGYT-----FTSYWWMWIRQPGQLEWIGG 50

QY 80 INPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSTSDTAMYICARADNYFDIVTGYT 139

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Db 51 INPSNGTNYNEKFKSKATLTVDKSSSATYMQLSPTSEDSAVYYCARWDYEGD----- 104
QY 140 SHYFDYWGRTLVTVSS 156
Db 105 -RYFDVWGTGTTTVTVSS 120

Search completed: April 5, 2004, 13:24:55
Job time : 7.1269 secs


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QY 121 AMYCARADNYFDIVTGYTSHYEDYNGRGLTVTSS 156
DB 111 AIYFCARGNLGRGFGY--NWDPMGHGLTVTSS 144

RESULT 2
Q96GA6 Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851.1; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 60.7%; Score 508; DB 4; Length 614;
Best Local Similarity 65.0%; Pred. No. 8.1e-42;
Matches 104; Conservative 15; Mismatches 17; Indels 24; Gaps 4;

QY 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSD 119
DB 50 YRYLHWVRQAPGQALEWNGWITFPNGNTNYAQFQDRVITDRSMNTAYMELSLRSED 109
QY 120 TAMYCARADNYFDIVTGYTSHY---FDYNGRGLTVTSS 156
DB 110 TAMYCAR-----GYSSWDADFIDWGQGTMTVTVSS 140

RESULT 3
Q9BRV0 Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Prostate;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
Hypothetical protein.

Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC005951.1; AAH05951.1; -.
DR HSPF; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 60.2%; Score 503.5; DB 4; Length 500;
Best Local Similarity 65.0%; Pred. No. 1.7e-41;
Matches 102; Conservative 11; Mismatches 33; Indels 11; Gaps 2;

QY 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGY-----AFHT 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSD 120
DB 51 YSIIHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMTDTSTVYMELESLRSD 110
QY 121 AMYCARA-DNYFDIVTGYTSHYFDYNGRGLTVTSS 156
DB 111 AVYCARRYCSQNDYIYYNDYVMDVWGKGTITVTVSS 147

RESULT 4
Q7Z7P5 Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Rana S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullady S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettaman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko V.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield V.S.;
RA Krzywinski M.I.; Skalska U.; Small D.E.; Scherch A.; Schein J.B.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
Hypothetical protein.
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SQ SEQUENCE 469 AA; 51395 MW; C8D5B21BAAF795C CRC64;
Query Match 59.0%; Score 493.5; DB 4; Length 469;
Best Local Similarity 64.1%; Pred. No. 1.6e-40;
Matches 100; Conservative 13; Mismatches 26; Indels 17; Gaps 3;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSGASGHIFTA 60
DB 1 MDWTWRIFLVAAATGAHPQVHLVQSGAEVKKPGASVLSCKTSQYN-----FSS 50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRLTSDDT 120
DB 51 YDIWVROAPQGQLEWGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRLTSDDT 110
QY 121 AMYICARADNYFDIVTGYTSHFYDYGRTLVTVSS 156
DB 111 ALFYCATKSR-----GQVGD-FDSWQGLTVTVSS 139
RESULT 5
ID Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE IG VH protein precursor (Fragment).
GN IG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT 19G4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor".
RL Blood 92:496-506(1998).
DR HSSP; P01772; 2FB4.
DR EMBL; AJ224083; CAAL1829.1; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
Query Match 58.9%; Score 493; DB 4; Length 150;
Best Local Similarity 63.5%; Pred. No. 4e-41;
Matches 99; Conservative 10; Mismatches 27; Indels 20; Gaps 2;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSGASGHIFTA 60
DB 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKTSQYN-----LTE 50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRLTSDDT 120
DB 51 LPVHWVQAPGQLEWVSGFDPESGESIYAREFGVQSTVMTADTSTDIAYMELSLRLSDDT 110
QY 121 AMYICARADNYFDIVTGYTSHFYDYGRTLVTVSS 156
DB 111 AVYICAVPD-----PDAFDIWGGTMTVTVSS 136
RESULT 6
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Q96QSO
ID Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV039025; AAK82649.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537EB881FAF02 CRC64;
Query Match 58.5%; Score 489.5; DB 4; Length 159;
Best Local Similarity 60.4%; Pred. No. 9.5e-41;
Matches 96; Conservative 17; Mismatches 33; Indels 13; Gaps 2;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSGASGHIFTA 60
DB 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGSN-----50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRLTSDDT 120
DB 51 YTMWVROAPQGQPEWGMVGNPSPGSGARSYQKQFQRLTMDTSTVYMDLSRLSDDT 110
QY 121 AMYICARADNYF---DIVTGYTSHFYDYGRTLVTVSS 156
DB 111 AVYICAREWEITFGGAVSKGFFYYGMDVWGQGTMTVTVSS 149
RESULT 7
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;
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01-OCT-2003 (TREMBLrel. 25, Last annotation update)
WH1 protein precursor (Fragment).
WH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005570; CAA06599.1; -
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT SIGNAL.
FT NON_TER
FT SEQUENCE 1 21
FT 157
FT SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
Query Match 56.8%; Score 475; DB 4; Length 157;
Best Local Similarity 58.3%; Pred. No. 2.6e-39;
Matches 91; Conservative 20; Mismatches 29; Indels 16; Gaps 2;
QY 1 MDWTRILLFLVAATAGAHSGVQLVQSGAEVKKPGASVKVSCTGSGYNFTGYSASGHIFTA 60
DB 1 MDWTRVFLCLVAAPGVHSGVQLVQSGAEIKRPGASVKVCHTSGY-----VFIS 50
QY 61 YGVHWVRQAPQGQLEWNGMRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSRUTSDDT 120
DB 51 YYIHWVRQPRGQLEWNGGIGPGVSGTCAEKFQGSGLTTRNTTITVTVMELSLRFEDT 110
QY 121 AMYICARADNFDIVTGVTSYHYDYGRTGLTVSS 156
DB 111 AYYFCGRGRW-----RSGNYNGHWGQGPVTSS 140
RESULT 10
Q96DK0 PRELIMINARY; PRT; 496 AA.
ID Q96DK0 PRELIMINARY;
AC Q96DK0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ25298.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Gastric mucosa;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Houta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Osakuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR

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DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;

Query Match
Best Local Similarity 55.7%; Score 466.5; DB 4; Length 496;
Matches 93; Conservative 18; Mismatches 31; Indels 15; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSGVQLVSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAAATGAHSGVQLVSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLWGMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRISDDT 120
DB 51 YAFWTRQAPGQGLWGMGIIENFGAPNVAQFQDRVIAADSTTTVMELTSLTFEDT 110
QY 121 AMYICARADNYFDIVTGYTSHYF-DYWGRTGLTVTSS 156
DB 111 AFYICGRGLTY----GSGSYLLQHWGQGLTVTSS 143

RESULT 11
Q9UL92 PRELIMINARY; PRT; 124 AA.
ID Q9UL92
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
DE Homo sapiens (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., van der Merwe P.B., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035022; AAD56258.1; -.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 124 124
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match
Best Local Similarity 54.9%; Score 459.5; DB 4; Length 124;
Matches 91; Conservative 12; Mismatches 21; Indels 13; Gaps 2;

QY 20 QVQLVSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLWGMGR 79
DB 1 EVQLVSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLWGMGI 50
QY 80 INPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRISDDTAMYYICARADNYFDIVTGYT 139
DB 51 INPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRISDDTAMYYICARADNYFDIVTGYT 139
QY 140 SHYFDYWGRTGLTVTSS 156
DB 108 FSRFDYWGQGLTVTSS 124

us-10-044-569b-6.rspt
RESULT 12
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1810060009RIK protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN=CS7BL/6J; TISSUE=Pancreas;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL EMBL; AK007918; BAB25349.1; -.
DR PIR; S26746; S26746.
DR HSP; P01842; 2PB4.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; ig-like.
DR InterPro; IPR003006; ig_MHC.
DR InterPro; IPR003596; ig_V.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR SEQUENCE 473 AA; 51699 MW; 9DE57A514475FBB CRC64;

Query Match
Best Local Similarity 54.7%; Score 458; DB 11; Length 473;
Matches 85; Conservative 25; Mismatches 28; Indels 18; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSGVQLVSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MENSWFLLLSVTAGVHCQVQLKQSGAELVKPGASVKISKASGYTFD----- 50
QY 61 YSVHWVRQAPGQGLWGMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRISDDT 120
DB 51 YYINWVRQAPGQGLWGMGKIGPGSGSYNKEKFKRATLTADKSSSTAYVQLSLTSEDS 110
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTGLTVTSS 156
DB 111 AVYFCAR-----SGDYDFWYWGQGLTVTSSA 138

RESULT 13
Q921K1 PRELIMINARY; PRT; 278 AA.
ID Q921K1
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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CC This sequence represents the heavy chain variable region of the
 CC monoclonal antibody (WAB), KR1X1. This WAB produced by the cell line of
 CC the invention, specifically recognises the wild type factor VIII light
 CC chain. KR1X1 can be used to inhibit the binding of factor VIII to von
 CC Willebrand factor in a dose dependant manner. The new cell line KR1X1,
 CC is deposited with the Belgian Coordinated Collections of Micro-organisms,
 CC under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally
 CC with a thrombolytic agent, are useful for the treatment and/or prevention
 CC of hemostasis, coagulation disorder or thrombotic pathologic condition
 CC such as intravascular coagulation, arterial thrombosis, arterial
 CC restenosis, venous thrombosis or arteriosclerosis, and attenuation of
 CC coagulation in a mammal. An effective and safe antithrombotic therapy is
 CC provided which reduces the risk of bleeding in mammals, more particularly
 CC in humans

XX Sequence 156 AA;

Query Match 100.0%; Score 837; DB 4; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3.7e-71; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 DB 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 QY 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFGQVMTMSRDTISITAYMELSLTSDDT 120
 DB 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFGQVMTMSRDTISITAYMELSLTSDDT 120
 QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
 DB 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 2

AAO18878
 ID AAO18878 standard; protein; 156 AA.

XX AAO18878;

DT 07-NOV-2002 (first entry)

DE Human KR1X1 heavy chain variable region.

XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 42..64
 FT /label= CDR1
 FT Region 79..95
 FT /label= CDR2
 FT Region 128..145
 FT /label= CDR3

XX EPI222929-A2.

XX 17-JUL-2002.

XX 11-JAN-2002; 2002EP-00447005.

XX 11-JAN-2001; 2001US-0261405P.

XX (COLL-) COLLEN RES FOUND VZW D.

XX Jacquemin MG, Saint-Remy JR;

XX WPI; 2002-610270/66.

DR N-PSDB; AAL49256.

XX Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.

XX Disclosure; Fig 12; 41pp; English.

XX The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the heavy chain variable region of KR1X1

XX Sequence 156 AA;

Query Match 100.0%; Score 837; DB 5; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3.7e-71; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 DB 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 QY 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFGQVMTMSRDTISITAYMELSLTSDDT 120
 DB 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFGQVMTMSRDTISITAYMELSLTSDDT 120
 QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
 DB 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 3

ADE28427
 ID ADE28427 standard; protein; 471 AA.

XX ADE28427;

DT 29-JAN-2004 (first entry)

XX Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.

DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region heavy chain; 21-2-1.

XX Homo sapiens.

XX WO2003040170-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0346980P.

XX (PFIZ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX N-PSDB; ADE28426.

XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.

XX Claim 1; SEQ ID NO 34; 177pp; English.

PS The invention relates to a novel chimeric or human monoclonal antibody or

XX its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody variable region heavy chain protein of the invention.

XX Sequence 471 AA;

Query Match 73.1%; Score 611.5; DB 7; Length 471;

Best Local Similarity 76.9%; Pred. No. 2.8e-49;

Matches 120; Conservative 7; Mismatches 18; Indels 11; Gaps 2;

QY 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

Db 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDDT 120

Db 51 YNHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDDT 110

QY 121 AMYTCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

Db 111 AVYTCAR-DQPLGCTNGVCSYFDYWGQGLTVTVSS 145

RESULT 4

AAU74296

ID AAU74296 standard; protein; 470 AA.

XX AAU74296;

AC AAU74296;

DT 12-MAR-2002 (first entry)

DE Anti-human AILIM monoclonal antibody clone Umab-136, heavy chain.

XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antiallergic; antitumor; neuroprotective; antithyroid; vasotrophic;

KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;

KW activation inducible lymphocyte immunomodulatory molecule; AILIM;

KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;

KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;

KW allergic contact-type dermatitis; chronic inflammatory dermatosis;

KW systemic lupus erythematosus; autoimmune disorder; inflammation;

KW graft versus host reaction; immune rejection; intestinal immunity;

KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

XX Homo sapiens.

OS Homo sapiens.

XX WO200187981-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-JP004035.

XX 18-MAY-2000; 2000JP-00147116.

PR 30-MAR-2001; 2001JP-00099508.

XX (NISR) JAPAN TOBACCO INC.

XX Tsuji T, Tezuka K, Hori N;

XX WPI; 2002-075313/10.

DR N-PSDB; AAS99472.

PT New human monoclonal antibody that binds to activation inducible

PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid

PS arthritis, multiple sclerosis and inflammation.

XX Claim 30; Page 264-266; 300pp; English.

XX The invention relates to a novel human antibody (I), preferably a human

CC monoclonal antibody which binds to an activation inducible lymphocyte

CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal

CC transduction into a cell mediated by AILIM, for modulating proliferation

CC of AILIM-expressing cells, for modulating production of a cytokine from

CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity

CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of

CC AILIM-expressing cells. (I) is useful for treating, preventing or

CC prophylaxis of delayed type allergy. (I) is useful for treating and

CC preventing various diseases associated with AILIM-mediated costimulatory

CC transduction, and for inhibiting the onset and/or advancement of the

CC diseases. (I) is useful for suppression, prevention and/or treatment of

CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,

CC allergic contact-type dermatitis, chronic inflammatory dermatosis,

CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,

CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus

CC host reaction, graft versus host disease, immune rejection, disorders

CC caused by abnormal intestinal immunity, specifically inflammatory

CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,

CC nephritis, vasculitis, and pancreatitis. (I) induces no serious

CC immunorejection due to antigenicity to human, i.e., human anti-mouse

CC immunorejection (HAMA) in a host. AAU74296-AAU74301 represent anti-human

CC AILIM monoclonal antibody amino acid sequences of the invention

XX Sequence 470 AA;

SQ

Query Match 72.5%; Score 607; DB 5; Length 470;

Best Local Similarity 76.3%; Pred. No. 7.5e-49;

Matches 119; Conservative 9; Mismatches 16; Indels 12; Gaps 2;

QY 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

Db 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDDT 120

Db 51 YNHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDDT 110

QY 121 AMYTCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

Db 111 AVYTCAR--TYVDSGYYHDAFDINGQGTMTVTVSS 144

RESULT 5

AAW22841

ID AAW22841 standard; protein; 146 AA.

XX AAW22841;

AC AAW22841;

DT 12-SEP-1997 (first entry)

DE Human anti-tumour antigen antibody heavy chain variable region.

XX Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;

KW variable region; medicine; pharmacology; biochemistry; CDR;

KW complementarity determining region.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19 /label= sig_peptide

FT Peptide 20..146 /label= mat_peptide

FT Region 50..54 /label= CDR_1

FT Region 69..85

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FT Region /label= CDR_2
FT 118..1139
FT /label= CDR_3
XX
PN JP09100300-A.
PD 15-APR-1997.
XX
PF 03-OCT-1995; 95JP-00278266.
XX
PR 03-OCT-1995; 95JP-00278266.
XX
PA (HAGI/) HAGIWARA Y.
XX
DR WPI; 1997-276726/25.
DR N-PSDB; AAT75422.
XX
XX Anticancer human monoclonal antibody variable region sequences - and
PT related DNA and RNA.
XX
PS Claim 3; Page 10; 14pp; Japanese.
XX
CC The present sequence is a human anti-tumour antigen monoclonal antibody
CC (Mab) heavy chain variable region, useful in medicine, pharmacology and
CC biochemistry. The isotype of a Mab secreted by the human/human hybridoma
CC HT was determined to be mu and kappa. Human Mab was purified, and the
CC antigen recognised by human Mab CLN"-IgM identified by western blotting
XX
XX Sequence 146 AA;
SQ
Query Match 70.0%; Score 586; DB 2; Length 146;
Best Local Similarity 72.8%; Pred. No. 1.8e-47;
Matches 118; Conservative 6; Mismatches 12; Indels 26; Gaps 4;
QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKASGYTFG----- 50
QY 61 YSVHWVQAPQGLEWMGRINPNSGATDYAHKFGQVMTSRDTSISTAYMELSLTSDDT 120
DB 51 YYHWVQAPQGLEWMGRINPNSGGTNYAQKFGQVMTTRDTSISTAYMELSLRSDT 110
QY 121 AMYCARADNVFDIVTG---TGHYFDY-----WGRGLV 152
DB 111 AVYICARGPK-----GYCSTSCYFDYVYGGVMDVWGQGTTV 146
RESULT 6
AAB36215
ID AAB36215 standard; protein; 236 AA.
XX
AC AAB36215;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-13.
XX
KW Human; immune system associated protein; HISAP-13; immune disorder;
XX infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;

```

```

PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR N-PSDB; AAC6531.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
XX Claim 1; Col 71-72; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, mvasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 236 AA;
Query Match 65.8%; Score 550.5; DB 4; Length 236;
Best Local Similarity 70.7%; Pred. No. 7.2e-44;
Matches 111; Conservative 13; Mismatches 14; Indels 19; Gaps 4;
QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGY-----IITS 50
QY 61 YSVHWVQAPQGLEWMGRINPNSGATDYAHKFGQVMTSRDTSISTAYMELSLTSDDT 120
DB 51 YAMHWVQAPQGLEWMGRINAGNNTKYSQFGRTITRTDTSASTAYMELSLRSDT 110
QY 121 AMYCARADNVFDIVTG-YTSHYFDYWGRTLVTVSS 156
DB 111 AVYICAR-----VMAGEFTS--FDYWGQGLTVTVSS 139
RESULT 7
AAR66296
ID AAR66296 standard; protein; 117 AA.
XX
AC AAR66296;
XX
DT 25-MAR-2003 (revised)
DT 07-AUG-1995 (first entry)
XX
DE Human immunoglobulin variable heavy chain #2.
XX
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
XX cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX
OS Homo sapiens.
XX
PN WO9426895-A1.
XX
PD 24-NOV-1994.
XX
PF 10-MAY-1993; 93WO-JP000603.
XX
PR 10-MAY-1993; 93WO-JP000603.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Honjo T, Matsuda F;
XX
DR WPI; 1995-006791/01.
DR N-PSDB; AAQ78940.
XX
XX DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts.
PT
XX

```

PS Disclosure; Page 32-33; 130pp; Japanese.

XX Protein sequences (AAR6295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; CC Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh CC genes. The fragments cover a region of 800 kb. The DNA fragments were CC isolated from high molecular weight DNA from human placenta. The DNA was CC partially digested with TaqI restriction enzyme. The fragments were CC separated by gel electrophoresis and 35-45 kb fractions were collected. CC The fragments were ligated with ClaI-digested cosmid vector pJB81. The CC ligation products were in vitro packed and infected into E.coli 490A. The CC fragments were then subcloned by colony hybridisation. The Vh genes and CC the DNA fragments encoding them are useful in producing human CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN CC field.)

XX SQ Sequence 117 AA;

Query Match 65.7%; Score 550; DB 2; Length 117;

Best Local Similarity 83.5%; Pred. No. 3.5e-44;

Matches 106; Conservative 4; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRIELFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

DB 1 MDWTWRIELFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 120

DB 51 YYNHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 110

QY 121 AMYICAR 127

DB 111 AVYICAR 117

RESULT 8

AAAY96295

ID AAY96295 standard; protein; 148 AA.

AC AAY96295;

XX 16-AUG-2000 (first entry)

DE Human IGFAM-7 immunoglobulin.

XX Human; immunoglobulin; IGFAM-7; IGFAM; immune disorder; cancer;

KW infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= signal_peptide

FT Protein 20..148

FT /label= IGFAM-7

FT Domain 34..117

FT /label= Ig_domain

XX WO2000295583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

PI

PI Lu DM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

DR N-PSDB; AAA27387.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with PT altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 83; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein IGFAM-7. Its gene was isolated from a cDNA library of bladder tumour CC tissue. It is expressed in reproductive, gastrointestinal and immune CC haematopoietic tissue, where cancer and inflammation are common. The CC gene, protein, its antibodies, agonists and antagonists are suitable for CC diagnosing and treating many diseases, including cancer, immune system CC disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, hepatitis, CC disease, diabetes mellitus, emphysema, Graves' disease, scleroderma, CC systemic sclerosis, psoriasis, rheumatoid arthritis, complications of CC cancer, haemodialysis and extracorporeal circulation, trauma and CC haematopoietic cancer (such as leukaemia) and infections caused by CC bacteria, viruses, fungi or parasites

XX SQ Sequence 148 AA;

Query Match 65.4%; Score 547.5; DB 3; Length 148;

Best Local Similarity 68.6%; Pred. No. 7.9e-44;

Matches 107; Conservative 11; Mismatches 19; Indels 19; Gaps 2;

QY 1 MDWTWRIELFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

DB 1 MDWTWRIELFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 120

DB 51 YYNHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 110

QY 121 AMYICARADNYFDIVTGYTSHYFDYVGRGLTVTVSS 156

DB 111 AIYYCARGD-----YGNLHMGQGNLTVTVSS 137

RESULT 9

ABP57367

ID ABP57367 standard; protein; 145 AA.

AC ABP57367;

XX 22-APR-2003 (first entry)

DE Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.

XX Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;

KW antibody therapy.

XX Homo sapiens.

XX Synthetic.

XX WO200294880-A1.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-JP004816.

XX 18-MAY-2001; 2001JP-00150213.

XX 09-AUG-2001; 2001JP-00243040.

XX 11-OCT-2001; 2001JP-00314489.

XX (KIRI) KIRIN BEER KK.

XX

PI Mori E, Kataoka S;
 XX WPI; 2003-120790/11.
 DR N-PSDB; AB259698.
 XX
 PT New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
 PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
 PT nor inducing injury to hepatocytes, for use in therapy of malignant
 PT tumor.
 PT
 XX Claim 54; Page 62; 92pp; Japanese.
 PS
 CC The present invention describes antibodies or their functional fragments
 CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
 CC have cytostatic and apoptotic activities, and can be used in antibody
 CC therapy. The antibodies can be applied as remedies and preventives of
 CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
 CC in the therapy of malignant tumours. Remedies produced with the
 CC antibodies are highly safe, and avoid hepatotoxicity. The present
 CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
 CC present invention
 CC
 XX Sequence 145 AA;
 SQ
 Query Match 65.1%; Score 544.5; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 1.5e-43;
 Matches 109; Conservative 14; Mismatches 16; Indels 23; Gaps 3;
 QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
 DB 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYFTN----- 50
 QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDT 120
 DB 51 YKINWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDT 110
 QY 121 AMYCARADNYFDIVTGYTHYFDY-----WGRGLTVTVSS 156
 DB 111 AVYTCARS-----YCGSGYRDYGYGMDVWGQGLTVTVSS 145
 RESULT 10
 AAB53510
 ID AAB53510 standard; protein; 146 AA.
 XX
 AC AAB53510;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1050.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; anti-infective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200005351-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005883.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX

DR WPI; 2000-587534/55.
 DR N-PSDB; AAC98267.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.
 XX
 PS Claim 11; Page 1631; 2104pp; English.
 XX
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, anti-infective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX Sequence 146 AA;
 SQ
 Query Match 64.6%; Score 540.5; DB 3; Length 146;
 Best Local Similarity 67.5%; Pred. No. 3.6e-43;
 Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;
 QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
 DB 6 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTS 55
 QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDT 120
 DB 56 YDINWVRQATGQGLEWVGWVWNPNSANTGYAQKFGQGVTVTRNTSISTAYMELSLRSED 115
 QY 121 AMYCARADNY-----FDIVTGYTHYFDYWGRLTVTV 154
 DB 116 AVYTCARXRRLWELGMMWD-----FDYWGQGLTVTV 146
 RESULT 11
 AAB58464
 ID AAB58464 standard; protein; 476 AA.
 XX
 AC AAB58464;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Monoclonal antibody 4B5 heavy chain variable region.
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
 KW diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
 KW lung carcinoma; metastasis; anti-idiotypic antibody; GD2 antigen; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9902545-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 08-JUL-1998; 98WO-IB001046.
 XX
 PR 08-JUL-1997; 97US-0051945P.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Dan MD;
 XX
 XX WPI; 1999-120769/10.
 DR

DR N-PSDB; AAX06951.
XX New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for prophylactic
PT therapy to reduce risk of recurrence.
XX
XX
XX Claim 1; Page 79-80; 83pp; English.
XX
XX This polypeptide comprises the heavy chain variable region of the
CC recombinant human monoclonal antibody (MAB), 4B5. 4B5 recognises
CC antibodies specific for GD2 antigen antibodies. Antibodies specific for
CC GD2 recognise various cancers including glioblastoma, neuroblastoma,
CC malignant and/or metastatic melanoma, breast adenocarcinoma, lung
CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
CC immunologic specificity for antibodies specific for GD2. These
CC derivatives, or antigen binding fragments, comprise regions of the 4B5
CC VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include
CC Fab, F(ab')₂, Fab', scFv and isolated heavy and light chains (see also
CC AAX06951). Polynucleotide fragments (see AAX06951-54) encoding 4B5
CC antibody V regions are also provided, and therapeutic plasmids and
CC vectors, including vaccinia virus vectors, comprising these
CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
CC useful in generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g. astrocytoma,
CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural
CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
CC large cell lung adenocarcinomas, squamous cell carcinoma,
CC bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
CC transitional squamous cell carcinoma of the bladder, B and T cell
CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
XX
XX Sequence 476 AA;
SQ
Query Match 64.5%; Score 540; DB 2; Length 476;
Best Local Similarity 68.6%; Pred. No. 1.6e-42;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;
QY 1 MDWTWRLFLVAAATGASHQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHFTFA 60
DB 1 MDWTWRLFLVAAATGASHQVQLVQSGAEVKKPGASVKVSCKASGTT-----FTS 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSRLTSDPT 120
DB 51 FDLNWRVQAPGQGLEWMGMWNPNSGKTGYAQKFGQGRVTMTNTSTINTAYMELSGLRSEDT 110
QY 121 AMYYCAR-ADNYFDIVGTSHYP--DYWGRGTLTVSS 156
DB 111 AVYFCARNADN---VENAAIYHYGYMDVWGQGTITVSS 146
RESULT 12
ID ASP45711 standard; protein; 250 AA.
XX ASP45711;
AC ASP45711;
XX
XX 19-AUG-2002 (first entry)
XX Human Blys binding scFv SEQ ID 1722.
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
OS

XX WO200202641-A1.
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-027379P.
PR 25-MAY-2001; 2001US-0293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
PT
XX Claim 1; Page 2457-2458; 3149pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX Sequence 250 AA;
SQ
Query Match 64.4%; Score 539; DB 5; Length 250;
Best Local Similarity 75.9%; Pred. No. 9.4e-43;
Matches 104; Conservative 10; Mismatches 13; Indels 10; Gaps 1;
QY 20 QVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHFTAYSVHWVRQAPGQGLEWMGR 79
DB 1 QVQLQSGAEVKKPGASVKVSCKASGYTFTG-----YYHWVRQAPGQGLEWMGW 50
QY 80 INPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSRLTSDTAMYYCARADNYFDIVGT 139
DB 51 INPNSGGTNYAQKFGQGRVTMTNTSTSTAYMELSRLTSDTAVYYCARVLPHYLITGYS 110
QY 140 SHYEDYNGRGTLTVSS 156
DB 111 QNWFDPMGRGLTVSS 127
RESULT 13
ID AAY24370 standard; protein; 149 AA.
XX AAY24370;
AC AAY24370;
XX
XX 17-SEP-1999 (first entry)
XX Human monoclonal antibody against CtGF SEQ ID NO:8.
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
KW

KW cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
XX rheumatic vascular inflammation.
OS Homo sapiens.
XX WO9933878-A1.
XX PD 08-JUL-1999.
XX 16-DEC-1998; 98WO-JP005697.
XX 25-DEC-1997; 97JP-00367699.
XX 13-DEC-1998; 98JP-00356183.
XX PA (NISR) JAPAN TOBACCO INC.
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
XX WPI; 1999-430232/36.
XX N-PSDB; AAX90021.
XX New monoclonal antibody reactive with connective tissue growth factor
PT useful in the treatment of cell proliferation disorders.
XX Claim 17; Page 177-178; 212pp; Japanese.
XX AAX90020 to AAX90029 encode monoclonal antibodies which react with human
CC connective tissue growth factor (CTGF). AAX24369 to AAX24378 represent
CC these monoclonal antibodies. The antibodies are useful in the diagnosis,
CC prevention and treatment of cell proliferation disorders in which CTGF is
CC implicated, including fibrosis of lung, kidney, liver and other tissues;
CC liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis;
CC rheumatic vascular inflammation; hepatitis; and cancer
XX SQ Sequence 149 AA;
Query Match 63.6%; Score 532; DB 2; Length 149;
Best Local Similarity 68.6%; Pred. No. 2.3e-42;
Matches 107; Conservative 9; Mismatches 26; Indels 14; Gaps 2;
QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKAFTL-----HLSPG 51
Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKAFTL-----HLSPG 51
QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFGQRTVMSRDTISITAYWELSLRLSDDT 120
Db 52 YNHWVRQAPGQGLEWMGRIINPNSGATDYAHKFGQRTVMSRDTISITAYWELSLRLSDDT 111
QY 121 AMYYCARADNYFDIVGTSHYFDYWGRTLVTVSS 156
Db 112 AVYYCAR-----EGIAAAAIYGMVWGQGTTLTVSS 142
RESULT 14
AAU31804
ID AAU31804 standard; protein; 746 AA.
XX AC AAU31804;
XX 18-DEC-2001 (first entry)
XX Novel human secreted protein #2295.
XX Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX Homo sapiens.
XX WO200179449-A2.
XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US008656.
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX Claim 20; Page 511; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX SQ Sequence 746 AA;
Query Match 63.3%; Score 529.5; DB 4; Length 746;
Best Local Similarity 68.8%; Pred. No. 2.8e-41;
Matches 108; Conservative 9; Mismatches 23; Indels 17; Gaps 3;
QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGTYFTNNGLA----- 58
Db 5 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGTYFTNNGLA----- 58
QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFGQRTVMSRDTISITAYWELSLRLSDDT 120
Db 59 -----WVRQAPGQGLEWMGRIINPNSGATDYAHKFGQRTVMSRDTISITAYWELSLRLSDDT 114
QY 121 AMYYCAR-ADNYFDIVGTSHYFDYWGRTLVTVSS 156
Db 115 AVYYCAREKDN-----ATGAWFAYWGQGTTLTVSS 145
RESULT 15
AAU80290
ID AAU80290 standard; peptide; 135 AA.
XX AC AAU80290;
XX 30-MAY-2000 (first entry)
XX Humanised anti-Fas antibody heavy chain variable region SEQ ID NO:10.
XX Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
KW diagnosis; CDR; complementarity determining region; apoptosis;
KW immunosuppressive.
XX Homo sapiens.
XX Mus sp.
XX JP2000014383-A.
XX FN

PD 18-JAN-2000.
XX
XX PF 03-JUL-1998; 98JP-00204318.
XX
XX PR 03-JUL-1998; 98JP-00204318.
XX
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
XX DR WPI; 2000-199626/18.
XX
XX PT Novel recombinant antibody used for treating and diagnosing autoimmune
PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX PS Claim 13; Page 13; 25pp; Japanese.
XX
XX CC The present invention describes a recombinant antibody (A) which binds to
CC fas antigen, and controls and induces apoptosis in cells which expressed
CC fas antigen. The complementarity determining regions (CDR) of (A) contain
CC amino acid sequences obtained from a mammal other than human, other
CC regions contain amino acid sequences from human and they partly contain
CC modified amino acids. (A) has immunosuppressive activity. (A) is used for
CC treating and/or diagnosing autoimmune diseases. The present sequence
CC represents a specifically claimed heavy chain variable region of (A)
XX
SQ Sequence 135 AA;

Query Match 63.1%; Score 528.5; DB 3; Length 135;
Best Local Similarity 66.9%; Pred. No. 4.4e-42;
Matches 105; Conservative 12; Mismatches 17; Indels 23; Gaps 3;

QY 1 MDWTWRIILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFD----- 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYWEISRLTSDDT 120
DB 51 YNHWVRQAPGQGLEWIGYIYPYNGGTGYNQKPKATSTRDTISITAYWEISRLTSEDS 110

QY 121 AMYYCARADNYFDIVTGYTSHY-FDYWGRGTLVTSS 156
DB 111 AMYYCAR-----SYAMDYWGQGTITVTSS 135

Search completed: April 5, 2004, 13:24:17
Job time : 51.4162 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 36.6904 Seconds
 (without alignments)
 1116.513 Million cell updates/sec

Title: US-10-044-569B-6
 Perfect score: 837
 Sequence: 1 MDWTRILLFLVAATGAHSQ.....GYTSHYFDYMGRTIVTVSS 156

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	837	100.0	156 14	US-10-044-569B-6	Sequence 6, Appli
2	607	72.5	470 9	US-09-859-053-28	Sequence 28, Appli
3	540.5	64.6	146 9	US-09-925-299-1050	Sequence 1050, Ap
4	540.5	64.6	146 10	US-09-925-299-1050	Sequence 1050, Ap
5	540	64.5	476 9	US-09-747-669-3	Sequence 3, Appli
6	540	64.5	476 14	US-10-290-703-3	Sequence 3, Appli
7	539	64.4	250 10	US-09-880-748-1722	Sequence 1722, Ap
8	532	63.6	149 14	US-10-390-986-8	Sequence 8, Appli
9	527	63.0	250 10	US-09-880-748-1723	Sequence 8, Appli
10	525.5	62.8	146 14	US-10-390-986-12	Sequence 12, Appli
11	525.5	62.8	256 10	US-09-880-748-1640	Sequence 1640, Ap
12	523.5	62.5	139 10	US-09-269-921-123	Sequence 123, Appl
13	523.5	62.5	139 10	US-09-509-098-46	Sequence 46, Appl
14	523.5	62.5	139 14	US-10-218-253-123	Sequence 123, Appl
15	523.5	62.5	146 14	US-10-390-986-10	Sequence 10, Appli

16	522.5	62.4	432	12	US-10-389-223A-10	Sequence 10, Appl
17	522.5	62.4	480	12	US-10-389-223A-4	Sequence 4, Appli
18	522.5	62.4	601	12	US-10-380-438-3	Sequence 3, Appli
19	522.5	62.4	614	12	US-10-389-223A-2	Sequence 2, Appli
20	522.5	62.4	658	12	US-10-380-438-1	Sequence 1, Appli
21	520.5	62.2	197	15	US-10-264-049-4263	Sequence 4263, Ap
22	520.5	62.2	249	10	US-09-880-748-1635	Sequence 1635, Ap
23	519.5	62.1	139	10	US-09-269-921-108	Sequence 108, App
24	519.5	62.1	139	10	US-09-269-921-115	Sequence 115, App
25	519.5	62.1	139	10	US-09-509-098-16	Sequence 16, Appl
26	519.5	62.1	139	10	US-09-509-098-30	Sequence 30, Appl
27	519.5	62.1	139	14	US-10-218-253-108	Sequence 108, App
28	519.5	62.1	139	14	US-10-218-253-115	Sequence 115, App
29	518.5	61.9	139	10	US-09-269-921-124	Sequence 124, App
30	518.5	61.9	139	10	US-09-509-098-48	Sequence 48, Appl
31	518.5	61.9	139	14	US-10-218-253-124	Sequence 124, App
32	518.5	61.9	247	10	US-09-880-748-1729	Sequence 1729, App
33	517.5	61.8	139	9	US-09-760-723-7	Sequence 7, Appli
34	517.5	61.8	139	9	US-09-355-925-7	Sequence 7, Appli
35	517.5	61.8	139	10	US-09-269-921-121	Sequence 121, App
36	517.5	61.8	139	10	US-09-269-921-125	Sequence 125, App
37	517.5	61.8	139	10	US-09-509-098-42	Sequence 42, Appl
38	517.5	61.8	139	10	US-09-509-098-50	Sequence 50, Appl
39	517.5	61.8	139	14	US-10-315-125-7	Sequence 7, Appli
40	517.5	61.8	139	14	US-10-218-253-121	Sequence 121, App
41	517.5	61.8	139	14	US-10-218-253-125	Sequence 125, App
42	517.5	61.8	139	14	US-10-428-085-7	Sequence 7, Appli
43	516.5	61.7	139	10	US-09-269-921-109	Sequence 109, App
44	516.5	61.7	139	10	US-09-269-921-118	Sequence 118, App
45	516.5	61.7	139	10	US-09-509-098-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-10-044-569B-6
 ; Sequence 6, Application US/10044569B
 ; Publication No. US20030175268A1
 ; GENERAL INFORMATION:
 ; APPLICANT: D. Colleen Research Foundation vzw
 ; APPLICANT: Jacquemin, Marc G
 ; APPLICANT: Saint-Remy, Jean-Marie R
 ; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
 ; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
 ; FILE REFERENCE: C1968
 ; CURRENT FILING DATE: 2002-01-11
 ; CURRENT APPLICATION NUMBER: US/10/044,569B
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR FILING DATE: 2001-01-11
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (124)..(192)
 ; OTHER INFORMATION: complementary determining region number one
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (232)..(285)
 ; OTHER INFORMATION: complementary determining region number two
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (282)..(435)
 ; OTHER INFORMATION: complementary determining region number three
 ; US-10-044-569B-6

Query Match 100.0%; Score 837; DB 14; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3,3e-75;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 2
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match 72.5%; Score 607; DB 9; Length 470;
Best Local Similarity 76.3%; Pred. No. 7.8e-52;
Matches 119; Conservative 9; Mismatches 16; Indels 12; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 144

RESULT 3
US-09-925-299-1050
; Sequence 1050, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0
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; SEQ ID NO 1050
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1050

Query Match 64.6%; Score 540.5; DB 9; Length 146;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
Db 6 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYT-----FTS 55
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 56 YDINWVRQATCGGLEWVGMNPNNSANTGYAQKFGRTVTRNTSISTAYMELSLRLSDEDT 115
QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTLVTV 154
Db 116 AVYICARRRWELLGMMWD-----FDYWGQGLILTV 146

RESULT 4
US-09-925-299-1050
; Sequence 1050, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1050
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1050

Query Match 64.6%; Score 540.5; DB 10; Length 146;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQVNTFTGYSASGHIFTA 60
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QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 56 YDINWVRQATCGGLEWVGMNPNNSANTGYAQKFGRTVTRNTSISTAYMELSLRLSDEDT 115
QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTLVTV 154
Db 116 AVYICARRRWELLGMMWD-----FDYWGQGLILTV 146

RESULT 5
US-09-747-669-3
; Sequence 3, Application US/09747669
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; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-747-669-3

Query Match          64.5%; Score 540; DB 9; Length 476;
Best Local Similarity 88.6%; Pred. No. 3.5e-45;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;

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QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSDDT 120
DB 1 MDWTWRVLFVLAATARSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSDDT 120
DB 1 MDWTWRVLFVLAATARSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
QY 121 AMYICAR-ADNYFDIVTGYTSHYP--DYWGRGLTVTVSS 156
DB 111 AVYFCARNADN---VEMAAIHYHYGMDVWGQGTITVTVSS 146

; RESULT 6
; US-10-290-703-3
; Sequence 3, Application US/10290703
; Publication No. US20030118593A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-10-290-703-3

Query Match          64.5%; Score 540; DB 14; Length 476;
Best Local Similarity 68.6%; Pred. No. 3.5e-45;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;
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QY 1 MDWTWRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
DB 1 MDWTWRVLFVLAATARSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSDDT 120
DB 1 MDWTWRVLFVLAATARSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
QY 51 FDLNWRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSDDT 110
DB 1 MDWTWRVLFVLAATARSQVLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTA 60
QY 121 AMYICAR-ADNYFDIVTGYTSHYP--DYWGRGLTVTVSS 156
DB 111 AVYFCARNADN---VEMAAIHYHYGMDVWGQGTITVTVSS 146

; RESULT 7
; US-09-880-748-1722
; Sequence 1722, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1722
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1722

Query Match          64.4%; Score 539; DB 10; Length 250;
Best Local Similarity 75.9%; Pred. No. 2.1e-45;
Matches 104; Conservative 10; Mismatches 13; Indels 10; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKTSYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
DB 1 QVQLQQSGAEVKKPGASVKVSCKASGYTFG-----YYMHWVRQAPGQGLEWMGW 50
QY 80 INPNSGATDYAHKFGQGVTVMSRDTSTAYMELSLRSDDTAMYICARADNYFDIVTGYT 139
DB 51 INPNSGGTNAQKPGQGVTVMTIRDTSTAYMELSLRSDDTAVYICARVLPHYDILTGYS 110
QY 140 SHYFDYWGRTGLTVTVSS 156
DB 111 QNWFDPMWGRGLTVTVSS 127

; RESULT 8
; US-10-390-986-8
; Sequence 8, Application US/10390986
; Publication No. US20030166011A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: JI-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
```

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; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-8

Query Match      63.6%; Score 532; DB 14; Length 149;
Best Local Similarity 68.6%; Pred. No. 5.7e-45;
Matches 107; Conservative 9; Mismatches 26; Indels 14; Gaps 2;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKAFWL-----HLSPG 51

QY 61 YSVHWVRQAPQGQLEWNGRINPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSLRSDTT 120
DB 52 YMHVVRQAPQGQLEWNGRINPNSGTHYAQMFQGRVTVTTRDTSTSTAYMELSLRSDTT 111

QY 121 AMYICARADNYFDIVTGYTSHYFDYGRGTLTVSS 156
DB 112 AVYICAR-----EGIAAAAIYGMVWGQGTIVTVSS 142

RESULT 9
US-09-880-748-1723
; Sequence 1723, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1723
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1723

Query Match      63.0%; Score 527; DB 10; Length 250;
Best Local Similarity 73.0%; Pred. No. 3.3e-44;
Matches 100; Conservative 14; Mismatches 13; Indels 10; Gaps 1;

QY 20 QVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSASGHIFTAYSVHWVRQAPQGQLEWNGR 79
DB 1 EVQLQSGAEVKPKGASVKVCKASGYTFG-----YMHVVRQAPQGQLEWNGW 50

QY 80 INPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSLRSDTTAMYICARADNYFDIVTGYT 139
DB 51 INPNSGATDYAHKFGQGRVTMTTRDTSTSTAYMELSLRSDTTAVYICARVLPHYDILTVS 110

QY 140 SHYFDYGRGTLTVSS 156
DB 111 QNWFDPWKGKGMVTVSS 127

```

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RESULT 10
US-10-390-986-12
; Sequence 12, Application US/10390986
; Publication No. US20030166011A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-12

Query Match      62.8%; Score 525.5; DB 14; Length 146;
Best Local Similarity 67.3%; Pred. No. 2.5e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps 2;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSASGHIFTA 60
DB 1 MDCWRIFLVAAATGTHAQVQLVQSGAEVKPKGASVKVCKVGYT-----LIE 50

QY 61 YSVHWVRQAPQGQLEWNGRINPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSLRSDTT 120
DB 51 LSMHWVRQAPKGLEWNGSFPDGETIYIAQFGQGRVTMTEDTSTDTAYMELSLRSED 110

QY 121 AMYICARADNYFDIVTGYTSHYFDYGRGTLTVSS 156
DB 111 AVYICATS-----TVVTPWYFDYWGQGLTVTVSS 139

RESULT 11
US-09-880-748-1640
; Sequence 1640, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1640

Query Match      62.8%; Score 525.5; DB 10; Length 256;
Best Local Similarity 74.3%; Pred. No. 4.7e-44;
Matches 104; Conservative 8; Mismatches 15; Indels 13; Gaps 2;

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QY 20 QVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQLEWNGR 79
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGYFTG-----YYMHWVRQAPGQLEWNGW 50
QY 80 INPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDTAMYYCARADNYFDIVTGY- 138
Db 51 INPNSGGTNYAQKFGQWVTMTSDTISITAYMELSLRSEDTAVYYCARAGSYDILTGY 110
QY 139 --TSHYEDYWGRTGLTVTVSS 156
Db 111 RPEDGYFDYWGRTGLTVTVSS 130

RESULT 12

US-09-269-921-123
; Sequence 123, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; EARLIER FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 123
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region
; OTHER INFORMATION: version p
US-09-269-921-123

Query Match 62.5%; Score 523.5; DB 10; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
Db 51 YMWQWVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTAYMELSLRSED 110
QY 121 AMYCARADNYFDIVTGYTSHYEDYWGRTGLTVTVSS 156
Db 111 AVYYCARG-----LRRG--GYFDYWGQGTITTVTVSS 139

RESULT 13

US-09-509-098-46
; Sequence 46, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053456/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02

; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized H chain V
; OTHER INFORMATION: region (version p) of anti-HM 1.24 antibody
US-09-509-098-46

Query Match 62.5%; Score 523.5; DB 10; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
Db 51 YMWQWVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTAYMELSLRSED 110
QY 121 AMYCARADNYFDIVTGYTSHYEDYWGRTGLTVTVSS 156
Db 111 AVYYCARG-----LRRG--GYFDYWGQGTITTVTVSS 139

RESULT 14

US-10-218-253-123
; Sequence 123, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 123
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region
; OTHER INFORMATION: version p
US-10-218-253-123

Query Match 62.5%; Score 523.5; DB 14; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
Db 51 YMWQWVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTAYMELSLRSED 110

QY 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
|:||||| | :|||||:|||||
Db 111 AVTYCARG-----LRRG--GYFDYWGQGTIVTVSS 139

RESULT 15

US-10-390-986-10
; Sequence 10, Application US/10390986
; Publication No. US2003016601A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-10

Query Match 62.5%; Score 523.5; DB 14; Length 146;
Best Local Similarity 67.3%; Pred. No. 3.9e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps 2;

QY 1 MDWTWRIFLVAATGAHSQVLVQSGAEVKPGASVKVCKTSQGYNFTGYSASGHIFTA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDCTWRIFLVAATGTHAQVLVQFGAEVKPGASVKVCKVSGYT-----LFE 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTSTAYNELSLTSDT 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 51 LSMHWVRQAPGKGLWNGSFDPEDGETIYAKFGQGRVTMTEDTSTDTAYNELSLRSED 110
QY 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
|:||||| | :|||||:|||||
Db 111 AVTYCATS-----TVVTPWYFDYWGQGTIVTVSS 139

Search completed: April 5, 2004, 13:59:14
Job time : 37.6904 secs

CLASSIFICATION	536
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US/08/137,117
FILING DATE:	20-DEC-1993
APPLICATION NUMBER:	WO PCT/JP92/00544
FILING DATE:	24-APR-1992
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	JP 4-32084
FILING DATE:	19-FEB-1992
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	JP 3-95476
FILING DATE:	25-APR-1991
ATTORNEY/AGENT INFORMATION:	
NAME:	WEGNER, Harold C.
REGISTRATION NUMBER:	25,258
REFERENCE/DOCKET NUMBER:	53466/126/AAOK
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(202)672-5300
TELEFAX:	(202)672-5399
TELEX:	904136
INFORMATION FOR SEQ ID NO:	112:
SEQUENCE CHARACTERISTICS:	
LENGTH:	135 amino acids
TYPE:	amino acid
TOPOLOGY:	linear
MOLECULE TYPE:	protein
US-08-436-717-112	

Query Match	62.2%	Score 520.5	DB 2	Length 135
Best Local Similarity	65.4%	Pred. No. 7.6e-46		
Matches 102	Conservative 13	Mismatches 20	Indels 21	Gaps 2

Qy	1	MDMTWRLFLVAAATGAHSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60
Db <th>1</th> <th>MDMTWRFVFLAVAGAHLSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60</th>	1	MDMTWRFVFLAVAGAHLSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60

Qy	61	YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSTISTAYMELSLTSDDT 120
Db <th>51</th> <th>YVHWVRQAPGQRLWMMGYIDPFGNGTSYNQKFKGRVITVDTASTAYMELSLTSDDT 110</th>	51	YVHWVRQAPGQRLWMMGYIDPFGNGTSYNQKFKGRVITVDTASTAYMELSLTSDDT 110

Qy	121	AMVYCARADNYFDIVGTYSHYFDYWGRTLVTVSS 156
Db <th>111</th> <th>AVYICARGGN-----RFAYWQGLTVTVSS 135</th>	111	AVYICARGGN-----RFAYWQGLTVTVSS 135

RESULT 9	US-08-513-968-38
Sequence 38	Application US/08513968
Patent No.	6114143
GENERAL INFORMATION:	
APPLICANT:	EDA, Yasuyuki
APPLICANT:	MAEDA, Hiroaki
APPLICANT:	MAKIZUMI, Keiichi
APPLICANT:	SHIOSAKI, Kouichi
APPLICANT:	OSATOMI, Kiyoshi
APPLICANT:	KINACHI, Kazuhiko
APPLICANT:	HIGUCHI, Hirofumi
APPLICANT:	TOKIYOSHI, Sachio
TITLE OF INVENTION:	ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES:	86
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	BROWDY AND NEIMARK
STREET:	419 Seventh Street, N.W., Suite 300
CITY:	Washington
STATE:	D.C.
COUNTRY:	USA
ZIP:	20004
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
OPERATING SYSTEM:	IBM PC compatible
SOFTWARE:	Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/436,717
FILING DATE:	

APPLICATION NUMBER:	US/08/137,117D
FILING DATE:	20-DEC-1993
CLASSIFICATION:	530
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	WO PCT/JP92/00544
FILING DATE:	24-APR-1992
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	JP 4-32084
FILING DATE:	19-FEB-1992
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	JP 3-95476
FILING DATE:	25-APR-1991
ATTORNEY/AGENT INFORMATION:	
NAME:	WEGNER, Harold C.
REGISTRATION NUMBER:	25,258
REFERENCE/DOCKET NUMBER:	53466/126/AAOK
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(202)672-5300
TELEFAX:	(202)672-5399
TELEX:	904136
INFORMATION FOR SEQ ID NO:	112:
SEQUENCE CHARACTERISTICS:	
LENGTH:	135 amino acids
TYPE:	amino acid
TOPOLOGY:	linear
MOLECULE TYPE:	protein
US-08-137-117D-112	

Query Match	62.2%	Score 520.5	DB 1	Length 135
Best Local Similarity	65.4%	Pred. No. 7.6e-46		
Matches 102	Conservative 13	Mismatches 20	Indels 21	Gaps 2

Qy	1	MDMTWRLFLVAAATGAHSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60
Db <th>1</th> <th>MDMTWRFVFLAVAGAHLSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60</th>	1	MDMTWRFVFLAVAGAHLSQVQLVSGAEVKKPGASVKVSKCTSGYNFTGYSASGHIFTA 60

Qy	61	YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSTISTAYMELSLTSDDT 120
Db <th>51</th> <th>YVHWVRQAPGQRLWMMGYIDPFGNGTSYNQKFKGRVITVDTASTAYMELSLTSDDT 110</th>	51	YVHWVRQAPGQRLWMMGYIDPFGNGTSYNQKFKGRVITVDTASTAYMELSLTSDDT 110

Qy	121	AMVYCARADNYFDIVGTYSHYFDYWGRTLVTVSS 156
Db <th>111</th> <th>AVYICARGGN-----RFAYWQGLTVTVSS 135</th>	111	AVYICARGGN-----RFAYWQGLTVTVSS 135

RESULT 8	US-08-436-717-112
Sequence 112	Application US/08436717
Patent No.	5817790
GENERAL INFORMATION:	
APPLICANT:	TSUCHIYA, Masayuki
APPLICANT:	SATO, Koh
APPLICANT:	BENDIG, Mary
APPLICANT:	JONES, Steven
APPLICANT:	SALDANHA, Jose
TITLE OF INVENTION:	RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION:	INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES:	158
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Foley & Lardner
STREET:	3000 K Street, N.W., Suite 500
CITY:	Washington
STATE:	D.C.

APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: EDA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-968-38

Query Match 61.8%; Score 517.5; DB 3; Length 137;
Best Local Similarity 64.1%; Pred. No. 1.6e-45;
Matches 100; Conservative 15; Mismatches 22; Indels 19; Gaps 2;

QY 1 MDMTWRILFLVAATGAHSGVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDMTWRVFLAVAPGAHSGVQLVQSGAEVKKPGASVKYSCKASGYT-----FTE 50

QY 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDT 120
DB 51 YTHHWVRQAPGQGLEWIGGPNNGDTSYTKRFGKATMTVDTSITAYMELSLRSEDT 110

QY 121 AMYICARADNYFDIVTGYTSHYFDYWGGRGLTVTVSS 156
DB 111 AVYVCA-----TPYVAIDSGQGLTVTVSS 137

RESULT 10
US-09-355-925-7
Sequence 7, Application US/09355925
Patent No. 6503510
GENERAL INFORMATION:
APPLICANT: KOISHIHARA, YASUO
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 139
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of H chain V region version r of
OTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7

Query Match 61.8%; Score 517.5; DB 4; Length 139;
Best Local Similarity 66.0%; Pred. No. 1.6e-45;
Matches 103; Conservative 11; Mismatches 25; Indels 17; Gaps 3;

QY 1 MDMTWRILFLVAATGAHSGVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDMTWRVFLAVAPGAHSGVQLVQSGAEVKKPGASVKYSCKASGYT-----FTP 50

QY 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDT 120
DB 51 YTHHWVRQAPGQGLEWMSIFPGDTRYSQKFGRTMTADKSTSTAYMELSLRSEDT 110

QY 121 AMYICARADNYFDIVTGYTSHYFDYWGGRGLTVTVSS 156
DB 111 AVYVCA-----LRRG--GYFDYWGGRGLTVTVSS 139

RESULT 11
US-08-477-877B-94
Sequence 94, Application US/08477877B
Patent No. 5730979
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cecelia, Byrne, Bain, Gilfillan,
ADDRESS: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,877B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-477-877B-94

Query Match 61.6%; Score 516; DB 1; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 14; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWNGR 79
DB 1 QVQLVQSGAEVKKPGASVKYSCKASGYTFTG-----YMHVVRQAPGQGLEWNGR 50

QY 80 INPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLRSDTAMTYICARADNYFDIVTGYT 139
DB 51 INPNSGGTNYAQKFGQGRVTMTVDTSITAYMELSLRSDTAVYICARTEYIVV---- 106

Mon Apr 5 14:16:20 2004

us-10-044-569b-6.rai

Page 8

Search completed: April 5, 2004, 13:44:09
Job time : 14.9898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 11.6142 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-8
Perfect score: 738
Sequence: 1 METPAQLLFLLLLLPDTTG.....TKVEIKRTVAAPSVFIIPPSS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625.5	84.8	145	2 S20631	IG kappa chain - h
2	619	83.9	144	2 PL0106	IG kappa chain pre
3	608.5	82.5	129	1 K3HUHA	IG kappa chain pre
4	598.5	81.1	129	1 K3HUHI	IG kappa chain pre
5	596.5	80.8	129	2 S49532	anti-Sm antibody V
6	590.5	80.0	128	2 S20636	IG kappa chain V r
7	585.5	79.3	129	2 S46369	IG light chain var
8	585.5	79.3	134	2 S38643	IG kappa chain V r
9	576	78.0	129	2 S40325	IG kappa chain - h
10	572.5	77.6	129	2 A32274	IG kappa chain pre
11	570.5	77.3	130	2 S20637	IG kappa chain V r
12	569	77.1	131	2 S40346	IG kappa chain V-J
13	566.5	76.8	130	2 S40360	IG kappa chain - h
14	564	76.4	116	2 B27594	IG kappa chain pre
15	563.5	76.4	121	2 S40327	IG kappa chain - h
16	563.5	74.9	116	2 C27594	IG kappa chain pre
17	548.5	74.3	124	2 S20633	IG kappa chain - h
18	537	72.8	116	2 B2521	IG kappa chain pre
19	535	72.5	128	1 K3HU41	IG kappa chain pre
20	533.5	72.3	127	2 S40380	IG kappa chain pre
21	533.5	72.3	129	2 S40363	IG kappa chain V-J
22	532.5	72.2	215	2 A23746	IG kappa chain - h
23	531	72.0	129	2 S29627	IG kappa chain V-I
24	527	71.4	128	2 S40379	IG kappa chain V r
25	526	71.3	114	2 S40375	IG kappa chain V-J
26	525	71.1	125	2 S40344	IG kappa chain V-J
27	525	71.1	128	2 S40345	IG kappa chain V-J
28	524	71.0	128	2 A56701	IG kappa chain V r
29	519.5	70.4	215	2 JE0242	IG kappa chain NIG

ALIGNMENTS

RESULT 1

S20631
IG kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20631
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20631
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <LSE>
A:Cross-references: EMBL:Z11903; NID:G33156; PIDN:CAA77955.1; PID:G33157
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:36-111/Domain: immunoglobulin homology <IMW>

Query Match 84.8%; Score 625.5; DB 2; Length 145;
Best Local Similarity 86.0%; Pred. No. 1.3e-44;
Matches 123; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLPDTTGIVLTQSPGTLSPGERATLSCRASQVAVLAWYQOK 60
DB 1 METPAQLLFLLLLPDTTGIVLTQSPGTLSPGERATLSCRASQVAVLAWYQOK 60
QY 61 PGQAPRLIIYGASRATDIPHRFSGSGGTFTLTISRLEPEDFAVYVCOQYGTSLTF 120
DB 61 PGQAPSLVIYGVSRATGIDPRFSGSGSETDFTLTISRLEPEDFAVYVCHQGYTP-LTF 119
QY 121 GGGTKVEIKRTVAAPSVFIIPPSS 143
DB 120 GGGTKVEIKRTVAAPSVFIIPPSS 142

RESULT 2

PL0106
IG kappa chain precursor V-J-C region (LS1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: PL0106; MUID:89235583; PMID:2341221
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SLT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:1-20/Domain: signal sequence #status predicted <SIG>
P:21-115/Domain: V region <VRE>

```
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match      83.9%; Score 619; DB 2; Length 144;
Best Local Similarity 88.1%; Pred. No. 4.4e-44;
Matches 126; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||
Db 1 MEAPQQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOR 59
   |||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||
Db 60 PGQAPRLIIYDASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYCCQ-RSNWPLTF 118
   |||

QY 121 GGQTKVEIKRTVAAPSVFIFPPS 143
   |||
Db 119 GGQTKVEIKRTVAAPSVFIFPPS 141
   |||

RESULT 3
K3HUI
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0022
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      81.1%; Score 598.5; DB 1; Length 129;
Best Local Similarity 91.5%; Pred. No. 1.9e-42;
Matches 119; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||
Db 61 PGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119
   |||

QY 121 GGQTKVEIKR 130
   |||
Db 120 GGQTKVEIKR 129
   |||

RESULT 5
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49532
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <MAH>
A:Cross-references: EMBL:Z46345; NID:G560843; PID:CAA86464.1; PID:G560844
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 596.5; DB 2; Length 129;
Best Local Similarity 90.8%; Pred. No. 2.8e-42;
Matches 118; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||
```

```
RESULT 4
K3HUI
Ig kappa chain precursor V-III region (Hic) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0021
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0021
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      81.1%; Score 598.5; DB 1; Length 129;
Best Local Similarity 91.5%; Pred. No. 1.9e-42;
Matches 119; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||
Db 61 PGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119
   |||

QY 121 GGQTKVEIKR 130
   |||
Db 120 GGQTKVEIKR 129
   |||

RESULT 5
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49532
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <MAH>
A:Cross-references: EMBL:Z46345; NID:G560843; PID:CAA86464.1; PID:G560844
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 596.5; DB 2; Length 129;
Best Local Similarity 90.8%; Pred. No. 2.8e-42;
Matches 118; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||
```

Db 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 6

S20636
IG kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S20636
R/Lees: S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A/Reference number: S20631
A/Accession: S20636
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <BEN>
A/Cross-references: EMBL:Z11894; NID:G33200; PIDN:CAA77948.1; PID:G33201
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 590.5; DB 2; Length 128;
Best Local Similarity 91.5%; Pred. No. 8.7e-42;
Matches 118; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 119

QY 121 GGGTKVEIKR 129

Db 120 GGGTKVEIKR 128

RESULT 7

S46369
IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46369
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46369
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <BEN>
A/Cross-references: EMBL:Z27170
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 585.5; DB 2; Length 129;
Best Local Similarity 88.5%; Pred. No. 2.3e-41;
Matches 115; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 60

QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 8

S38643
IG kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38643
R/Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A/Reference number: S38643
A/Accession: S38643
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <BEN>
A/Cross-references: EMBL:Z27170; NID:G415955; PIDN:CAA81694.1; PID:G415956
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:41-116/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 585.5; DB 2; Length 134;
Best Local Similarity 88.5%; Pred. No. 2.3e-41;
Matches 115; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 1 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 6 METPAQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 65
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 66 PQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 124
QY 121 GGGTKVEIKR 130
Db 125 GGGTKVEIKR 134

RESULT 9

S40325
IG kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40325
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:9408091; PMID:8258341
A/Accession: S40325
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLE>
A/Cross-references: EMBL:X72435; NID:G441338; PIDN:CAA51103.1; PID:G441339
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:35-110/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 576; DB 2; Length 129;
Best Local Similarity 84.5%; Pred. No. 1.4e-40;
Matches 109; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 2 ETAPQLLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVASAYLAWYQOKP 61
Db 1 ETAPQLLLFLLMLPDPSPGQVLTQSPVLTSLSPGERATLSCRASQSVSSSYLAWYQORP 60
QY 62 GQAPRLIYGASSRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 121

Db 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGTSL-120

QY 122 GGTKEIKR 130

Db 121 PGTKVDIR 129

RESULT 10

A32274 Ig kappa chain precursor V-III region (EVI-15) - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000

C:Accession: A32274

R:Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.

J. Clin. Invest. 81, 1511-1516, 1988

A>Title: Complete protein sequences of the variable regions of the cloned heavy and light actors of the Wa idiotype family.

A:Reference number: A92767; MUID:88213701; PMID:2452836

A:Accession: A32274

A:Molecule type: DNA

A:Residues: 1-129 <NEW>

A:Cross-references: GB:M20031

A>Note: this sequence was determined from the codon GAT for residue 17 as Ala

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>

F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 77.6%; Score 572.5; DB 2; Length 129;

Best Local Similarity 89.2%; Pred. No. 2.6e-40;

Matches 116; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60

Db 1 METPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVSSNELAWYQOK 60

QY 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGTSL-120

Db 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGTSL-119

QY 121 GGTKEIKR 130

Db 120 GGTKEIKR 129

RESULT 11

S20637 Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S20637; S20632

R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A:Reference number: S20631

A:Accession: S20637

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <LEE>

A:Cross-references: EMBL:Z11890; NID:G33202; PIDN:CAA77944.1; PMID:333203; EMBL:Z11895; N

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 77.3%; Score 570.5; DB 2; Length 130;

Best Local Similarity 87.7%; Pred. No. 3.9e-40;

Matches 114; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60

Db 1 METPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVSSNELAWYQOK 60

QY 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGTSL-119

Db 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOHYGGSFRET 120

QY 120 FGGTKVEIK 129

Db 121 FGGTKLEIK 130

RESULT 12

S40346

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40346

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40346

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: EMBL:X72456; NID:9441380; PIDN:CAA51124.1; PID:9441381

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-110/Domain: immunoglobulin homology <IMW>

Query Match 77.1%; Score 569; DB 2; Length 131;

Best Local Similarity 84.0%; Pred. No. 5.2e-40;

Matches 110; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 ETPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOKP 61

Db 1 ETPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVSSSELAWYQHP 60

QY 62 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGTSL-121

Db 61 GQAPRLIIYGASRRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYVCHYXGSPPTFG 120

QY 122 GGTKEIKRTV 132

Db 121 GGTKEIKRTV 131

RESULT 13

S40360

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40360

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40360

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-130 <KLE>

A:Cross-references: EMBL:X72470; NID:9441408; PIDN:CAA51138.1; PID:9441409

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-111/Domain: immunoglobulin homology <IMW>

Query Match 76.8%; Score 566.5; DB 2; Length 130;

Best Local Similarity 86.9%; Pred. No. 8.3e-40;

Matches 113; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 2 ETPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60

Db 1 ETPAQLFLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSRASQSVSSSELAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGTSAALLTF 120
DB 61 PGQAPRLIYDASNRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGTSAALLTF 120
QY 121 GGGTKVEIKR 130
DB 121 GGGTKVEIKR 130

RESULT 14

B27594
IG kappa chain precursor V-III (Nalm-6) - human
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: B27594
J:Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.
J:Exp. Med. 167, 488-501, 1988
A:Title: The kappa-deleting element. Germline and rearranged, duplicated and dispersed
A:Reference number: A92779; MUID:88154739; PMID:3126251
A:Accession: B27594
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-116 <GRA>
A:Note: this sequence was translated from an aberrantly rearranged kappa gene from lambda
C:Genetics:
A:Map position: 2
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 564; DB 2; Length 116;
Best Local Similarity 94.8%; Pred. No. 1.2e-39;
Matches 109; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOK 60
QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGTSA 115
DB 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGS 115

RESULT 15

S40327
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40327
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40327
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72437; NID:G441342; PIDN:CAAS1105.1; PID:G441343
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-108/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 563.5; DB 2; Length 121;
Best Local Similarity 90.2%; Pred. No. 1.4e-39;
Matches 110; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 4 PAQLFLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOKPQ 63
DB 1 PAQLFLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQOKPQ 60
QY 64 APRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGTSAALLTFGG 123

DB 61 APRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYQYGS 119
QY 124 TK 125
DB 120 TR 121

Search completed: April 5, 2004, 13:43:03
Job time : 12.6142 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.533 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738

Sequence: 1 METPAQLFLLLWLPDITG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608.5	82.5	129	1	KV3L_HUMAN
2	598.5	81.1	129	1	KV3M_HUMAN
3	535	72.5	128	1	KV3K_HUMAN
4	531.5	72.0	129	1	KV3H_HUMAN
5	506.5	68.6	119	1	KV3I_HUMAN
6	503	68.2	116	1	KV3J_HUMAN
7	489.5	66.3	109	1	KV3E_HUMAN
8	489.5	66.3	109	1	KV3E_HUMAN
9	481.5	65.2	109	1	KV3D_HUMAN
10	464.5	62.9	109	1	KV3G_HUMAN
11	457.5	62.0	108	1	KV3A_HUMAN
12	456	61.8	100	1	KV3C_HUMAN
13	422.5	57.2	109	1	KV3F_HUMAN
14	417.5	56.6	123	1	KV4E_HUMAN
15	404	54.7	129	1	KV1W_HUMAN
16	399	54.1	134	1	KV4C_HUMAN
17	396.5	53.7	117	1	KV1J_HUMAN
18	393	53.3	131	1	KV2F_MOUSE
19	391.5	53.0	133	1	KV2F_MOUSE
20	379	51.4	129	1	KV1X_HUMAN
21	378	51.2	122	1	KV3E_MOUSE
22	378	51.2	149	1	KV5A_MOUSE
23	370	50.1	107	1	KV1Y_HUMAN
24	369.5	50.1	108	1	KV1D_HUMAN
25	367	49.7	108	1	KV1M_HUMAN
26	367	49.7	114	1	KV4A_HUMAN
27	365	49.5	128	1	KV5E_MOUSE
28	364	49.3	108	1	KV1H_HUMAN
29	363.5	49.3	121	1	KV40_HUMAN
30	358	48.5	136	1	KV5B_MOUSE
31	357	48.4	108	1	KV1F_HUMAN
32	356	48.2	108	1	KV1K_HUMAN
33	352	47.7	108	1	KV1S_HUMAN

34 350.5 47.5 117 1 KV1I_HUMAN P01601 homo sapien
35 350 47.4 108 1 KV1V_HUMAN P04430 homo sapien
36 347 47.0 108 1 KV1P_HUMAN P01608 homo sapien
37 345 46.7 108 1 KV1R_HUMAN P01610 homo sapien
38 344 46.6 108 1 KV1E_HUMAN P01597 homo sapien
39 342 46.3 108 1 KV1E_HUMAN P01604 homo sapien
40 341.5 46.3 117 1 KV2E_HUMAN P06309 homo sapien
41 341 46.2 111 1 KV3L_MOUSE P01664 mus musculus
42 341 46.2 111 1 KV3N_MOUSE P01666 mus musculus
43 340 46.1 108 1 KV1O_HUMAN P01609 homo sapien
44 340 46.1 111 1 KV3U_MOUSE P01673 mus musculus
45 339.5 46.0 109 1 KV1T_HUMAN P01612 homo sapien

ALIGNMENTS

RESULT 1

KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P00022; K3HUHA.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 82.5%; Score 608.5; DB 1; Length 129;

Best Local Similarity 93.1%; Pred. No. 7.5e-52;

Matches 121; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDITGTEIVLTQPPGTLSPGERATLSCRASQSVASVAYLWYQOK 60

Db 1 METPAQLFLLLWLPDITGTEIVLTQPPGTLSPGERATLSCRASQSVSSVYLAQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSLTLF 120


```
Db 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSP-RTF 119
QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 2
KV3M HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tonhave E., Chen P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P18021; K3HUH1.
DR HSSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 81.1%; Score 598.5; DB 1; Length 129;
Best Local Similarity 91.5%; Pred. No. 6.9e-51;
Matches 119; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSP-RTF 120
Db 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSP-WTF 119

QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 3
KV3H HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
```

```
KV3K HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combiato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; Z00021; CA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.5%; Score 535; DB 1; Length 128;
Best Local Similarity 85.4%; Pred. No. 9e-45;
Matches 111; Conservative 3; Mismatches 14; Indels 2; Gaps 2;

QY 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGESATLSCRASQSV-SSNLAWYQOK 59

QY 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSP-RTF 120
Db 60 RGQAPRLIRPASPANGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSP-YTF 118

QY 121 GGGTKVEIKR 130
Db 119 GGGTKLEIKR 128

RESULT 4
KV3H HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
```

DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177570; PubMed=3083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carlson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199 (1986).
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 CC
 CC EMBL; M12740; AA858992.1; -;
 CC HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR Pfam; PF00047; Ig_v.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
 Query Match 72.0%; Score 531.5; DB 1; Length 129;
 Best Local Similarity 82.3%; Pred. No. 2e-44;
 Matches 107; Conservative 6; Mismatches 16; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLWLPDPTTGTGEIVLTQPPGTLSPGERTATLSRASQSVASAYLAWYQOK 60
 DB 1 MEAPALLFLLLLWLPDPTTGTGEIVLTQSPATLSVSPGERATLSRASQSV-SNNLAWYQOK 59
 QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGDTFTLTISRLEPEDFVAVYCOQYQTSALLTF 120
 DB 60 PGQAPRLIYGASTRATGIPARFSGSGGDTFTLTISRQSEDFVAVYCOQYNNWPPWTF 119
 QY 121 GGQTKVEIKR 130
 DB 120 GGQTRVEIKR 129
 RESULT 5
 KV31_HUMAN STANDARD; PRT; 115 AA.
 ID KV31_HUMAN
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus."
 RL Nucleic Acids Res. 12:9229-9236 (1984).
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
 Query Match 68.6%; Score 506.5; DB 1; Length 115;
 Best Local Similarity 91.0%; Pred. No. 4.4e-42;
 Matches 101; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLWLPDPTTGTGEIVLTQPPGTLSPGERTATLSRASQSVASAYLAWYQOK 60
 DB 1 MEAPALLFLLLLWLPDPTTGTGEIVLTQSPATLSVSPGERATLSRASQSV-SSYLAWYQOK 59
 QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGDTFTLTISRLEPEDFVAVYCOQ 111
 DB 60 PGQAPRLIYGASTRATGIPARFSGSGGDTFTLTISRLEPEDFVAVYCOQ 110
 RESULT 6
 KV3J_HUMAN STANDARD; PRT; 116 AA.
 ID KV3J_HUMAN
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;

RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus."
RL Nucleic Acids Res. 12:9229-9236 (1984).
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSP: P80362; IWL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 68.2%; Score 503; DB 1; Length 116;
Best Local Similarity 87.4%; Pred. No. 9.7e-42;
Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 METAQALLFLLLLPDTTTEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQQK 60
DB 1 MEAPQALLFLLLLPDTTTEIVLTQPPGTLSPGERATLSGRASQSVSSYLTWYQQK 60

QY 61 PQQAPRLIYGASRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQ 111
DB 61 PQQAPRLIYGASRATSIPTARFSGSGSGTDFLTISRLEPEDFAVYCCQ 111

RESULT 7
KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01892; K3HUSI.

Query Match 68.2%; Score 503; DB 1; Length 116;
Best Local Similarity 87.4%; Pred. No. 9.7e-42;
Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 METAQALLFLLLLPDTTTEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQQK 60
DB 1 MEAPQALLFLLLLPDTTTEIVLTQPPGTLSPGERATLSGRASQSVSSYLTWYQQK 60

QY 61 PQQAPRLIYGASRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQ 111
DB 61 PQQAPRLIYGASRATSIPTARFSGSGSGTDFLTISRLEPEDFAVYCCQ 111

RESULT 7
KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01892; K3HUSI.

DR HSP: P80362; IWL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KW DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 66.3%; Score 489.5; DB 1; Length 109;
Best Local Similarity 88.2%; Pred. No. 1.8e-40;
Matches 97; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQQKPGQAPRLIYGASRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSGRASQSVSSYLTWYQQKPGQAPRLIYGASRATGIP 60

QY 81 HRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAITLTFGGTKVEIKR 130
DB 61 DRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAITLTFGGTKVEIKR 109

RESULT 8
KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region WOL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HUL.
DR HSP: P80362; IWL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KW DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CDEE CRC64;

Query Match 66.3%; Score 489.5; DB 1; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.8e-40;
Matches 99; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQQKPGQAPRLIYGASRATDIP 80
DB 1 EIVLTQPGTSLSPGERATLSGRASQSVSSYLTWYQQKPGQAPRLIYGASRATGIP 60

QY 81 HRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAITLTFGGTKVEIKR 130

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

RESULT 9

KV3D HUMAN STANDARD; PRT; 109 AA.

AC P01622;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region Ti.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=72188439; PubMed=5027703;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."

RT Hoppe-Seyler's Z. Physiol. Chem. 353:189-208 (1972).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A01895; K3HUT.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region Ti.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;

RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYG-SLGRTFGGTKVEIKR 109

reactivity with antipeptide antibodies.";

MOI. Immunol. 23:239-244 (1986).

DR PIR; A01893; K3HUGO.

DR HSP; P80362; IWL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=86230578; PubMed=3086710;</

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RESULT 12
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DR GO:0005576; C:extracellular; NAS.
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR GO:0003823; F:antigen binding; NAS.
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DR InterPro; IPR007110; Ig-like.
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR HSP; P80362; 1WTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Hybridoma.
FT NON_TER 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
FT SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 61.8%; Score 456; DB 1; Length 100;
Best Local Similarity 90.7%; Pred. No. 2.8e-37;
Matches 88; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 19 TGEVLVTFQPTLSLSPGERATLSGRASQSVASAYLAWYQKPGQAPRLIIYGASRATD 78
DB 3 SGEVLVTFQPTLSLSPGERATLSGRASQSVSSYLAWYQKPGQAPRLIIYGATSRATG 62

QY 79 IPHFGSGSGTDTLTISRLEPEDFAVYCCQYGTG 115
DB 63 IPDFFSGASGTDFTLTISRLEPEDFAVYCCQYGTG 99

RESULT 13
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DR GO:0005576; C:extracellular; NAS.
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR GO:0003823; F:antigen binding; NAS.
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DR InterPro; IPR007110; Ig-like.
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G.; Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.

DR PIR; A01897; K3HUPM.
DR HSP; P80362; 1WTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8AB86 CRC64;

Query Match 57.2%; Score 422.5; DB 1; Length 109;
Best Local Similarity 76.4%; Pred. No. 5.2e-34;
Matches 84; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 21 EIVTQPTLSLSPGERATLSGRASQSVASAYLAWYQKPGQAPRLIIYGASRATDIP 80
DB 1 EIVTQPTLSLSPGERATLSGRASQSVSSYLAWYQKPGQAPRLIIYGATSRATGIP 60

QY 81 HRFGSGSGTDTLTISRLEPEDFAVYCCQYGTG 130
DB 61 ARFGSGSGTDTLTISRLEPEDFAVYCCQYGTG 109

RESULT 14
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DR GO:0005576; C:extracellular; NAS.
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DR GO:0003823; F:antigen binding; NAS.
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G.; Bornkamm G.W.; Combriato G.; Mocikat R.; Pohlenz H.D.;
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germ-line gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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or send an email to license@ebi.ac.uk).
CC EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJI.
DR HSP; P80362; 1WTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 21 133
FT DOMAIN 21 43 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 44 60 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
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FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match
Best Local Similarity 56.68; Score 417.5; DB 1; Length 133;
Matches 84; Conservative 18; Mismatches 26; Indels 7; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPPGTLSPGERATLSCRASQSVASA-----YLA 55
Db 1 MWLQTVFISLLWISGAYGDIWVTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNVLA 60
QY 56 WYQKPGQAPRLIYGNASSRATDIPHRFSGSGSGTDFTLTISRLPEDFAVYCCQYGT 115
Db 61 WYQKPGQAPRLIYGNASSRATDIPHRFSGSGSGTDFTLTISRLPEDFAVYCCQYGT 119
QY 116 ALLTFGGGKVEIKR 130
Db 120 -IPTFGGKVEIKR 133

RESULT 15
KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC PIR; A01883; KIHUWK.
CC HSP; P01607; IREI.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
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FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 54.74; Score 404; DB 1; Length 129;
Matches 83; Conservative 15; Mismatches 29; Indels 2; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPPGTLSPGERATLSCRASQSVASAYLAWYCOQK 60
Db 3 MRVPAQLGLLLMLRGARCDIQTSFSSLSASVGDVTTTCRASQSI-SNYLWYCOQK 61
QY 61 PQGAPRLIYGNASSRATDIPHRFSGSGSGTDFTLTISRLPEDFAVYCCQYGTSAALLTF 120
Db 62 PKAPKLLIYAASSLSQSGVTSRFRSGSGSGTDFTLTISLQPEDSATYCCQ-SYSTLTITF 120
QY 121 GGGTKVEIK 129
Db 121 QGGTRLEIK 129
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Search completed: April 5, 2004, 13:24:56
Job time : 7.533 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 30.4873 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-8
Perfect score: 738
Sequence: 1 METPAQLFLLLMLPDTTG.....TKVEIKRTVAAPSVFIIPPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	505.5	68.5	109	Q9UL78	Q9ul78 homo sapien
2	483.5	65.5	109	Q9UL86	Q9ul86 homo sapien
3	479	64.9	234	Q7Z473	Q7z473 homo sapien
4	460.5	62.4	239	Q8NEK0	Q8nek0 homo sapien
5	455	61.7	236	Q7Z3V4	Q7z3v4 homo sapien
6	443.5	60.1	229	Q8TCD0	Q8tcd0 homo sapien
7	436.5	59.1	109	Q9UL85	Q9ul85 homo sapien
8	418	56.6	237	Q7SZ36	Q7sz36 xenopus lae
9	415	56.2	238	Q99M37	Q99m37 mus musculus
10	413	56.0	238	Q8VC16	Q8vc16 mus musculus
11	411	55.7	108	Q9UL83	Q9ul83 homo sapien
12	407	55.1	236	Q7TS98	Q7ts98 mus musculus
13	404	54.7	236	Q7TMK3	Q7tmk3 mus musculus
14	390.5	52.9	239	Q8K0F8	Q8k0f8 mus musculus
15	389	52.7	234	Q8VCP0	Q8vcp0 mus musculus
16	388.5	52.6	107	Q96SA9	Q96sa9 homo sapien

17	387.5	52.5	239	11	Q8VC55	Q8vc55 mus musculus
18	381	51.6	234	11	Q8R062	Q8r062 mus musculus
19	377	51.1	108	4	Q9UL77	Q9ul77 homo sapien
20	374	50.7	131	11	Q8LIC3	Q8lic3 mus musculus
21	374	50.7	234	11	Q9IWF8	Q9iwf8 mus musculus
22	367	49.7	108	4	Q9UL79	Q9ul79 homo sapien
23	367	49.7	233	11	Q9IWS9	Q9iws9 mus musculus
24	365.5	49.5	114	11	Q8K1F1	Q8k1f1 mus musculus
25	362.5	49.1	235	11	Q7TMK0	Q7tmk0 mus musculus
26	358.5	48.6	107	4	Q9UL81	Q9ul81 homo sapien
27	358	48.5	108	4	Q9UL70	Q9ul70 homo sapien
28	357	48.4	116	4	Q96PF6	Q96pf6 homo sapien
29	352	47.7	214	11	Q9RIA5	Q9ria5 mus musculus
30	346.5	47.0	235	11	Q9IWI2	Q9iwi2 mus musculus
31	345.5	46.8	112	11	Q8K1F3	Q8k1f3 mus musculus
32	344.5	46.7	112	11	Q8K1F2	Q8k1f2 mus musculus
33	336	45.5	111	11	Q920E9	Q920e9 mus musculus
34	335.5	45.5	134	11	Q8VDD0	Q8vdd0 mus musculus
35	331	44.9	298	11	Q9QYF0	Q9qyf0 mus musculus
36	330	44.7	108	11	Q8VIJ0	Q8vi j0 mus musculus
37	329	44.6	111	11	Q8I1U6	Q8i1u6 mus musculus
38	329	44.6	148	11	Q8K122	Q8k122 mus musculus
39	327.5	44.4	106	5	Q9U410	Q9u410 schistosoma
40	325	44.0	127	11	Q925S9	Q925s9 mus musculus
41	322	43.6	97	11	Q9UL76	Q9ul76 mus musculus
42	321.5	43.6	243	11	Q7TQM2	Q7tqm2 mus musculus
43	319	43.2	101	11	Q9UL78	Q9ul78 mus musculus
44	318.5	43.2	112	11	Q8K1F0	Q8k1f0 mus musculus
45	318	43.1	109	11	Q920E6	Q920e6 mus musculus

ALIGNMENTS

RESULT 1
Q9UL78 PRELIMINARY; PRT; 109 AA.
ID Q9UL78
AC Q9UL78; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30607; G30607.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.

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DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 1
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 68.5%; Score 505.5; DB 4; Length 109;
Best Local Similarity 91.8%; Pred. No. 6.3e-44;
Matches 101; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQKPGQAPRLIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYGASSRATGIP 60

QY 81 HRFSGSGGDTFTLTISRLPEDFAVYCCQYGTSAITFGGKTKVEIKR 130
Db 61 DRFSGSGGDTFTLTISRLPEDFAVYCCQYGTSAITFGGKTKVEIKR 109

RESULT 2
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=9614934;
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match 65.5%; Score 483.5; DB 4; Length 109;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 96; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQKPGQAPRLIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYGSSRATGIP 60

QY 81 HRFSGSGGDTFTLTISRLPEDFAVYCCQYGTSAITFGGKTKVEIKR 130
Db 61 DRFSGSGGDTFTLTISRLPEDFAVYCCQYGTSAITFGGKTKVDIKR 109

us-10-044-569b-8.rsppt

RESULT 3
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
MEDLINE=9614934;
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match 64.9%; Score 479; DB 4; Length 234;
Best Local Similarity 68.5%; Pred. No. 8.6e-41;
Matches 98; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSRASQSVASAYLAWYQK 60
Db 1 MRVPAQLGLLLMLPGARCAIRVTQSPSFSASTGDRVITCRASQSIGSYLAWYQK 59

QY 61 PQAPRLIYGASSRATDIPHRFSGSGGDTFTLTISRLPEDFAVYCCQYGTSAIT 120
Db 60 PKAPQLIYAASTLQSGVPSRFSASGDTFTLISCLSDPFAVYCCQYGTYP-WTF 118

QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 119 GGGTKVEIKRTVAAPSVFIFPPS 141

RESULT 4
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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Db 120 PSTFGGQTKLEIKRTVAAPSVEIFPPS 146
RESULT 7
Q9UL85 ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1843B7C7AFACCC CRC64;

Query Match 59.1%; Score 436.5; DB 4; Length 109;
Best Local Similarity 79.1%; Pred. No. 7e-37;
Matches 87; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSRASQSVASAVLAWYQKPGQAPRLIYGASSRATDIP 80
Db 1 EIVNTQPALVSPGERATLSRASQSI--SSNLAWYQKPGQAPRLIYGASTRATGIP 59
QY 81 HRFSGSGGTHFTLISRLEPEDFVAVYQYQYTSALLTFGGTKVEIKR 130
Db 60 ARFSGSGGTEFTLTISLSQSEDFALVHCQYNSWPPLTFGGTKVEIKR 109

RESULT 8
Q7SZ36 ID Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC Q7SZ36
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN RP SEQUENCE FROM N.A.

RC RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnarch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC054155; AAH54155.1; -.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47BD0D2639CB436 CRC64;

Query Match 56.6%; Score 418; DB 13; Length 237;
Best Local Similarity 62.9%; Pred. No. 1.5e-34;
Matches 88; Conservative 16; Mismatches 32; Indels 4; Gaps 2;

QY 7 LFFILLMLPDTTGEIVLTQPGTSLSPGERATLSRASQSV--SAYLAWYQKPGQ 63
Db 7 LFLPMLWLQSGYQIVLTQSPDYVSPGETVTLTKASSVAIGSTIYLHWYQKSGQ 66
QY 64 APRLLIYGASSRATDIPHRFSGSGGTHFTLISRLEPEDFVAVYQYQYTSALLTFGGG 123
Db 67 VPKLIIYLANTRHTGTPERISGSGSGTDTLTISRMEADADYVCOQ--SRSDPLTFGKG 125
QY 124 TKVEIKTVAAPSVEIFPPS 143
Db 126 TRVELKENDAKPAVFIKPS 145

RESULT 9
Q9NM37 ID Q9NM37 PRELIMINARY; PRT; 238 AA.
AC Q9NM37
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC020355; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
```



```
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9P9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 55.7%; Score 411; DB 4; Length 108;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

QY 21 EIVLTPPGTSLSPGERATLSRASQSVASVAYLAWYQKPGQAPPELLIYGASSRATDIP 80
DB 1 EIVWTSPTLSVSPERATLSRASQSV-SNNLAWYQKPGQAPPELLIYCASTRATGIP 59

QY 81 HRFSGSGGDFLTISRLEPEDFVAVYQQYQTSALLTFGGGKVEIKR 130
DB 60 ARFSGSGGTEFTLTISSLQFEDFVAVYQCHVNNWP-FTFGPGTKVDIKR 108

RESULT 12
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Henman J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -.
SQ SEQUENCE 236 AA; 26454 MW; 2C596EBF5EA10F4C CRC64;

Query Match
Best Local Similarity 55.1%; Score 407; DB 11; Length 236;
Matches 80; Conservative 23; Mismatches 38; Indels 2; Gaps 2;

QY 1 METPAQLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLAWYQK 60
DB 3 MRTPAQFLGILLWFPQWKCDIKWTQSPSSMYASLGERVTITCKASQDI-NSYLSWFQX 61

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGSDFTLTISRLEPEDFVAVYQQYQTSALLTF 120
DB 62 PGKSPKTLIYRANRLVDGVSPFRSGSGGQDYSLTSSLESDDTATYCLHQHESP-YTF 120

QY 121 GGGTKVEIKTVAAPSFIIPPS 143
DB 121 GGGTKLEIKRADAAPTYSIIPPS 143

RESULT 13
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Breast tumor;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055906; AAK55906.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03489AAA6396F CRC64;

Query Match
Best Local Similarity 54.7%; Score 404; DB 11; Length 236;
Matches 81; Conservative 21; Mismatches 39; Indels 2; Gaps 2;

QY 1 METPAQLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLAWYQK 60
DB 3 MRAPQFGLILLWFPQIRCDIKWTQSPSSMYASLGERVTITCKASQDIKS-YLSWYQK 61

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGSDFTLTISRLEPEDFVAVYQQYQTSALLTF 120
DB 62 PWKSPKTLIYATSLADGVSPFRSGSGGQDYSLTSSLESDDTATYCLHQHESP-YTF 120

QY 121 GGGTKVEIKTVAAPSFIIPPS 143
DB 121 GSGTKLEIKRADAAPTYSIIPPS 143

RESULT 14
Q8KOF8 PRELIMINARY; PRT; 239 AA.
AC Q8KOF8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAK31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
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Search completed: April 5, 2004, 13:42:06
JOB time : 30.4873 secs

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DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGC1; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00061; ADH_SHORT; 1.  
DR PROSITE: PS00835; IG_LIKE; 2.  
DR PROSITE: PS00290; IG_MHC; 1.  
KW Hypothetical protein_  
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;  
  
Query Match 52.7%; Score 389.5; DB 11; Length 234;  
Best Local Similarity 55.9%; Pred. No. 9.7e-32;  
Matches 80; Conservative 21; Mismatches 37; Indels 5; Gaps 2;  
  
QY 1 METPAQLFLLLLPDTTGTGEIVLTQPPGTLSPGERATLSCRASQSV-----ASAYLAW 56  
Db 1 MNGPAQLFLVLVLSIQINGDVVMTQPLTSLVTIGQASISCKSQSLFYNGKRYLSW 60  
  
QY 57 YQKPGQAPRLIYGASRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSA 116  
Db 61 LLQRPQGSPKRLISLVSKLDSGVDPDRFSGSGGTDFLTISRVEAEDLGVIYCLQ-STHF 119  
  
QY 117 LLTPGGTKVEIKRTVAAPSFIPTPS 143  
Db 120 PYTFGGTKLEIKRAADAAPTIVSIPTPS 146  
  
RESULT 15  
Q8VCP0 PRELIMINARY; PRT; 234 AA.  
AC Q8VCP0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg P.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019474; AAH19474.1; -.  
DR PIR; B47329; B47329.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;  
  
Query Match 52.7%; Score 389; DB 11; Length 234;  
Best Local Similarity 55.9%; Pred. No. 1.3e-31;  
Matches 80; Conservative 21; Mismatches 40; Indels 2; Gaps 2;  
  
QY 1 METPAQLFLLLLPDTTGTGEIVLTQPPGTLSPGERATLSCRASQSVASAYLAWYQK 60  
Db 1 MSVFTQVLGLLLCLTGARCDIQLTQSPASLSASVGETVITCRASENIYS-YLAWYQK 59  
  
QY 61 PQAPRLIYGASRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSA 120  
Db 60 QGKSPQLLVYNAKTLADGVPSRFGSGSGTQFSLKINSLOPEDFGSYCQH-SGIPFTF 118  
  
QY 121 GGGTKVEIKRTVAAPSFIPTPS 143  
Db 119 GSGTKLEIKRAADAAPTIVSIPTPS 141
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:09:21 ; Search time 46.2149 Seconds
(without alignments)
874.270 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738

Sequence: 1 METPAQLLELLMLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqp29Jan04:*
- 2: Geneseqp1980s:*
- 3: Geneseqp1980s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2000s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	738	100.0	143	4 AAB47061	Aab47061 Light cha
2	738	100.0	143	5 AAO18879	Aao18879 Human KRI
3	667	90.4	234	7 ADE28481	Ade28481 Human ant
4	666.5	90.3	235	3 AAY93702	Aay93702 The kappa
5	666.5	90.3	235	3 AAY93729	Aay93729 The kappa
6	666.5	90.3	235	6 AAE35884	Aae35884 Human 4.1
7	660	89.4	236	5 AAU74299	Aau74299 Anti-huma
8	658.5	89.2	235	6 ABP71366	Abp71366 Anti-OPGL
9	654.5	88.7	142	4 AAB47060	Aab47060 Light cha
10	654.5	88.7	142	3 AAO18877	Aao18877 Human B02
11	654.5	88.7	233	3 AAY93704	Aay93704 The kappa
12	654.5	88.7	233	3 AAY93731	Aay93731 The kappa
13	654.5	88.7	233	6 AAE35886	Aae35886 Human 4.8
14	652	88.3	236	5 AAU74301	Aau74301 Anti-huma
15	649.5	88.0	150	2 AAU0069	Aau0069 Human mon
16	649.5	88.0	150	4 AAE00946	Aae00946 Human mon
17	645	87.4	234	3 AAY93733	Aay93733 The kappa
18	645	87.4	234	3 AAY93708	Aay93708 The kappa
19	645	87.4	234	6 AAE35888	Aae35888 Human 6.1
20	641.5	86.9	150	7 ABU10485	Abu10485 Human C-a
21	627	85.0	234	7 ADE28473	Ade28473 Human ant
22	622	84.3	131	6 ABP57366	Abp57366 Anti-TRAI
23	619.5	83.9	130	6 ADA43061	Ada43061 Human ant
24	619.5	83.9	238	6 ABR41582	Abra41582 Human DIT
25	614	83.2	234	3 AAY92239	Aay92239 Human bon

ALIGNMENTS

RESULT 1

AAB47061

ID AAB47061 standard; protein; 143 AA.

XX

AC AAB47061;

XX

DT 08-MAY-2001 (first entry)

XX

DE Light chain variable region VL of KRIX1.

XX

KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;

KW complementarity determining region; CDR; WAB; BO2C11;

KW conformational epitope; factor VIII; KRIX1; von Willebrand factor;

KW hemostasis; intravascular coagulation; arterial thrombosis;

KW arterial restenosis; venous thrombosis; arteriosclerosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 43..54

FT Domain /label= CDR1

FT Domain 59..75

FT Domain /label= CDR2

FT Domain 109..118

FT Domain /label= CDR3

WO200104269-A1.

XX

PD 18-JAN-2001.

XX

XX 13-JUL-2000; 2000WO-EP006677.

XX

PR 14-JUL-1999; 99GB-00016450.

XX

PR 14-JUL-1999; 99US-C143891P.

XX

PA (LEUV-) LEUVEN RES & DEV VZW.

XX

XX Jacquemin MG, Saint-Remy JR;

PI

XX WPI; 2001-138333/14.

XX

DR N-PSDB; AAC85454.

XX

PT Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.

XX

PS Example 5; Fig 9; 55pp; English.

XX

Aag71272 Human gen.
Abg63490 Human alb.
Abj36930 Anti-CD40
Aaw11155 Anti-lung
Aar38672 vk325-Jk2
Adc61062 Human ant
Aao14066 Light cha
Abu08018 Human mon
Aar41286 F105 rear
Add01357 Human imm
Aar38673 F105VK-F1
Aam24101 Human EST
Aau33249 Novel hum
Aau14463 Human nov
Aau14461 Human nov
Aau14464 Human nov
Aab99378 Human int
Aab75011 Anti-IL8
Aab99397 Human int

CC This sequence represents the light chain variable region of the
 CC monoclonal antibody (WAb), KR1X1. This Mab produced by the cell line of
 CC the invention, specifically recognises the wild type factor VIII light
 CC chain. KR1X1 can be used to inhibit the binding of factor VIII to von
 CC Willebrand factor in a dose dependant manner. The new cell line KR1X 1,
 CC is deposited with the Belgian Coordinated Collections of Micro-organisms,
 CC under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally
 CC with a thrombolytic agent, are useful for the treatment and/or prevention
 CC of hemostasis, coagulation disorder or thrombotic pathologic condition
 CC such as intravascular coagulation, arterial thrombosis, arterial
 CC restenosis, venous thrombosis or arteriosclerosis, and attenuation of
 CC coagulation in a mammal. An effective and safe antithrombotic therapy is
 CC provided which reduces the risk of bleeding in mammals, more particularly
 CC in humans
 XX
 SQ Sequence 143 AA;

Query Match 100.0%; Score 738; DB 4; Length 143;
 Best Local Similarity 100.0%; Pred. No. 3e-47;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METPAQLLELLWLPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLELLWLPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLLIYGASRRATDIPHRFSGSGGTDFTLTISRLEPDPFVYCCQYGTGALLTF 120
 DB 61 PGQAPRLLIYGASRRATDIPHRFSGSGGTDFTLTISRLEPDPFVYCCQYGTGALLTF 120
 QY 121 GGGTKVEIKRTVAAPSVFIPTPPS 143
 DB 121 GGGTKVEIKRTVAAPSVFIPTPPS 143

RESULT 2
 AAO18879
 ID AAO18879 standard; protein; 143 AA.

XX AC AAO18879;
 XX DT 07-NOV-2002 (first entry)
 XX DE Human KR1X1 light chain variable region.
 XX KW Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antiinflammatory.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 43..54
 FT /label= CDR1
 FT Region 69..75
 FT /label= CDR2
 FT Region 108..117
 FT /label= CDR3

XX EP1222929-A2.
 XX 17-JUL-2002.
 XX 11-JAN-2002; 2002EP-00447005.
 XX 11-JAN-2001; 2001US-0261405P.
 XX (COLL-) COLLEN RES FOUND VZW D.
 XX Jacquemin MG, Saint-Remy JR;
 XX WPI; 2002-610270/66.

DR N-PSDB; AAL49257.
 XX Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.
 XX Disclosure; Fig 13; 41pp; English.
 XX The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the light chain variable region of KR1X1
 XX
 SQ Sequence 143 AA;

Query Match 100.0%; Score 738; DB 5; Length 143;
 Best Local Similarity 100.0%; Pred. No. 3e-47;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METPAQLLELLWLPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLELLWLPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLLIYGASRRATDIPHRFSGSGGTDFTLTISRLEPDPFVYCCQYGTGALLTF 120
 DB 61 PGQAPRLLIYGASRRATDIPHRFSGSGGTDFTLTISRLEPDPFVYCCQYGTGALLTF 120
 QY 121 GGGTKVEIKRTVAAPSVFIPTPPS 143
 DB 121 GGGTKVEIKRTVAAPSVFIPTPPS 143

RESULT 3
 ADE28481
 ID ADE28481 standard; protein; 234 AA.

XX AC ADE28481;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human anti-CD40 antibody 24-2-1 full length light chain protein.
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; light chain; 24-2-1.

XX OS Homo sapiens.
 XX WO2003040170-A2.
 XX 15-MAY-2003.
 XX 08-NOV-2002; 2002WO-US036107.
 XX 09-NOV-2001; 2001US-0348980P.

XX (PFIZ) PFIZER PROD INC.
 XX (ABGE-) ABGENIX INC.
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX WPI; 2003-441521/41.
 XX N-PSDB; ADE28480.
 XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.

XX Claim 7; SEQ ID NO 88; 177pp; English.

PS The invention relates to a novel chimeric or human monoclonal antibody or

XX its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

XX antibody full length light chain protein of the invention.

SQ Sequence 234 AA;

Query Match 90.4%; Score 667; DB 7; Length 234;

Best Local Similarity 92.3%; Pred. No. 8.3e-42;

Matches 132; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60

DB 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVSTYLAWYQOK 60

QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120

DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQY--SSLTFF 118

QY 121 GGCTKVEIKRTVAAPSVFIFPPS 143

DB 119 GPCTKVDIKRTVAAPSVFIFPPS 141

RESULT 4

AAAY93702

ID AAY93702 standard; protein; 235 AA.

AC AAY93702;

XX 03-OCT-2000 (first entry)

DT The kappa chain of immunoglobulin clone 4.1.1.

DE Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX WO200037504-A2.

PN 29-JUN-2000.

PD 23-DEC-1999; 99WO-US030895.

PF 23-DEC-1998; 98US-0113647P.

PR (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46865.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 1A; 157pp; English.

CC The present sequence represents a kappa chain of an antibody of the

CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)

CC -4. Antibodies of the invention are composed of a heavy chain variable

CC region, comprising a modified contiguous sequence from a FRI-PR3 sequence

CC encoded by a human VH3-33 family gene. The modifications are contained in

CC CDR1, CDR2 and/or framework regions. The antibodies may be used to

CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity

CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and

CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be

CC used to up-regulate immune system to up-regulate immunodeficient

CC disorders

XX Sequence 235 AA;

SQ Sequence 235 AA;

Query Match 90.3%; Score 666.5; DB 3; Length 235;

Best Local Similarity 91.6%; Pred. No. 9.1e-42;

Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60

DB 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSSSFLAWYQOR 60

QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120

DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119

QY 121 GGCTKVEIKRTVAAPSVFIFPPS 143

DB 120 GGCTKVEIKRTVAAPSVFIFPPS 142

RESULT 5

AAAY93729

ID AAY93729 standard; protein; 235 AA.

AC AAY93729;

XX 03-OCT-2000 (first entry)

DT The kappa chain of immunoglobulin clone 4.1.1.

DE Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX Key Location/Qualifiers

FF Peptide 1..20

FT /note= "signal peptide"

XX WO200037504-A2.

PN 29-JUN-2000.

PD 23-DEC-1999; 99WO-US030895.

PF 23-DEC-1998; 98US-0113647P.

PR (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46893.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 22g; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDRI, CDRI and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX

SQ Sequence 235 AA;
Query Match 90.3%; Score 666.5; DB 3; Length 235;
Best Local Similarity 91.6%; Pred. No. 9.1e-42;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
1 METPAQLLLFLLWLPTTGTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLWYQOK 60
1 METPAQLLLFLLWLPTTGTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLWYQOK 60
61 PGQAPRLIIYGASRRATDIPHRFSGSGSDFTLTISRLEPEDFAVYCCQYGTSP-WTF 120
61 PGQAPRLIIYGASRRATDIPHRFSGSGSDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119
121 GGGTKVEIKRTVAAPSVFIPTPS 143
120 GGGTKVEIKRTVAAPSVFIPTPS 142

RESULT 6
AAE35884
ID AAE35884 standard; protein; 235 AA.
AC AAE35884;
DT 17-JUN-2003 (first entry)
DE Human 4.1.1 anti-CTLA-4 antibody kappa chain.
KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW cancer.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..220
XX /label= Signal_peptide
XX Protein 21..235
XX /note= "Mature anti-CTLA-4 antibody kappa chain"
XX
XX EP1262193-A1.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253652.
XX
XX 23-MAY-2001; 2001US-0293042P.
XX
XX (PTIZ) PFIZER PROD INC.
XX
XX Hanson DC, Mueller EE;
XX
XX WPI; 2003-131215/13.
XX N-PSDB; AAD54344.
XX
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
XX preparation of medicament for the treatment of cancer.
XX Disclosure; Fig 1G; 76pp; English.
XX

CC The invention relates to the use of human anti-cytotoxic T lymphocyte
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC cancer, cancer of the anal region, stomach cancer, breast cancer,
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
XX The present sequence is human anti-CTLA-4 antibody kappa chain
SQ Sequence 235 AA;
Query Match 90.3%; Score 666.5; DB 6; Length 235;
Best Local Similarity 91.6%; Pred. No. 9.1e-42;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
1 METPAQLLLFLLWLPTTGTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLWYQOK 60
1 METPAQLLLFLLWLPTTGTGEIVLTQPPGTLSPGERATLSRASQSVASVAYLWYQOK 60
61 PGQAPRLIIYGASRRATDIPHRFSGSGSDFTLTISRLEPEDFAVYCCQYGTSP-WTF 120
61 PGQAPRLIIYGASRRATDIPHRFSGSGSDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119
121 GGGTKVEIKRTVAAPSVFIPTPS 143
120 GGGTKVEIKRTVAAPSVFIPTPS 142

RESULT 7
AAU74299
ID AAU74299 standard; protein; 236 AA.
XX
XX AAU74299;
DT 12-MAR-2002 (first entry)
DE Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW anti-allergic; antitumor; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatological; anti-inflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation;
KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX
XX Homo sapiens.
XX WO200187981-A2.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-JP004035.
XX
XX 18-MAY-2000; 2000JP-00147116.
XX 30-MAR-2001; 2001JP-00099508.
XX
XX (NISE) JAPAN TOBACCO INC.
XX
XX Tsuji T, Tezuka K, Hori N;
XX
XX WPI; 2002-075313/10.
XX N-PSDB; AAS99475.
XX
XX New human monoclonal antibody that binds to activation inducible
XX lymphocyte immunomodulatory molecule, useful for treating rheumatoid
XX arthritis, multiple sclerosis and inflammation.
XX
XX Claim 30; Page 284-285; 300pp; English.
XX
XX The invention relates to a novel human antibody (I), preferably a human

CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AIIIM, for modulating proliferation
 CC of AIIIM-expressing cells, for modulating production of a cytokine from
 CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AIIIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AIIIM-expressing cells. (II) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AIIIM-mediated costimulatory
 CC transduction, and for inhibiting the onset and/or advancement of the
 CC diseases. (I) is useful for suppression, prevention and/or treatment of
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
 CC host reaction, graft versus host disease, immune rejection, disorders
 CC caused by abnormal intestinal immunity, specifically inflammatory
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
 CC nephritis, vasculitis, and pancreatitis. (II) induces no serious
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
 CC AIIIM monoclonal antibody amino acid sequences of the invention

XX SQ Sequence 236 AA;

Query Match 89.4%; Score 660; DB 5; Length 236;
 Best Local Similarity 88.8%; Pred. No. 2.8e-41;
 Matches 127; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLFLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 DB 1 METPAQLFLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFAVYCCQYQTSALLTF 120
 DB 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFAVYCCQYQTSALLTF 120
 QY 121 GGGTKVEIKRTVAAPSVFIFFPPS 143
 DB 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

RESULT 8

ABP71366
 ID ABP71366 standard; protein; 235 AA.

XX AC ABP71366;

XX DT 28-APR-2003 (first entry)

XX DE Anti-OPGL-1 antibody kappa light chain.

XX KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
 XX KW antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Region /note= "IgG2 signal peptide"

FT Region 21..128

FT Region /note= "variable region"

FT Region 129..235

FT Region /note= "constant region"

XX WO2003002713-A2.

XX PD 09-JAN-2003.

XX PF 25-JUN-2002; 2002WO-US020181.

XX PR 26-JUN-2001; 2001US-0301172P.

XX XX

(ABGE-) ABGENIX INC.
 (AMGE-) AMGEN INC.

PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;

DR WI; 2003-210262/20.

DR N-PSDB; ABZ59148.

XX New antibodies that interact with osteoprotegerin ligands, useful for
 PT treating osteopneic disorders, e.g. osteoporosis, bone loss from
 PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
 PT osteonecrosis.

XX Claim 1; Fig 4; 144pp; English.

XX The invention relates to antibodies that interact with osteoprotegerin
 CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
 CC a biological sample. The antibody, or the pharmaceutical composition
 CC comprising the antibody, is also useful for treating osteopneic disorder,
 CC an inflammatory condition with attendant bone loss, an autoimmune
 CC condition with attendant bone loss in a patient or rheumatoid arthritis
 CC in a patient. In particular, the antibody or composition is useful for
 CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
 CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
 CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'
 CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
 CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
 CC kappa light chain

XX SQ Sequence 235 AA;

Query Match 89.2%; Score 558.5; DB 6; Length 235;

Best Local Similarity 91.6%; Pred. No. 3.6e-41;

Matches 131; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60

DB 1 METPAQLFLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60

QY 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFAVYCCQYQTSALLTF 120

DB 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFAVYCCQYQTSALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

DB 120 GGGTKVEIKRTVAAPSVFIFFPPS 142

RESULT 9

ABAB47060

ID AAB47060 standard; protein; 142 AA.

XX AC AAB47060;

XX DT 08-MAY-2001 (first entry)

XX DE Light chain variable region VL of B02C11.

XX KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;

XX KW complementarity determining region; CDR; Mab; B02C11;

XX KW conformational epitope; factor VIII; KRXL; von Willebrand factor;

XX KW hemostasis; intravascular coagulation; arterial thrombosis;

XX KW arterial restenosis; venous thrombosis; arteriosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 43..54

FT Domain /label= CDR1

FT Domain 69..75

FT Domain /label= CDR2

FT Domain 109..117

FT Domain /label= CDR3

XX WO200104269-A1.
 XX 18-JAN-2001.
 XX 13-JUL-2000; 2000WO-EP006677.
 XX 14-JUL-1999; 99GB-00016450.
 XX 14-JUL-1999; 99US-0143891P.
 XX (LEUV-) LEUVEN RES & DEV VZW.
 XX Jacquemin MG, Saint-Remy JR;
 XX WPI; 2001-138333/14.
 XX N-PSDB; AAC85453.
 PT Novel cell lines for producing monoclonal antibodies that bind to a
 FT factor involved in hemostasis and coagulation cascade, useful for
 FT treating and preventing coagulation disorders.
 XX
 PS Example 5; Fig 7; 55pp; English.
 CC This sequence represents the light chain variable region of the human
 CC monoclonal antibody (Mab), B02C11. B02C11 is a human Mab which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg215His factor
 CC VIII light chains. The Mab produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X 1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC hemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 CC
 XX SQ Sequence 142 AA;
 Query Match 88.7%; Score 654.5; DB 4; Length 142;
 Best Local Similarity 89.5%; Pred. No. 4.4e-41;
 Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITF 120
 DB 61 PGQAPRLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSA-ITF 119
 QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
 DB 120 GQGTREIKGTVAAPSVFIFPPS 142
 RESULT 10
 AA018877
 ID AA018877 standard; protein; 142 AA.
 XX AA018877;
 AC AA018877;
 XX 07-NOV-2002 (first entry)
 DT Human B02C11 light chain variable region.
 DE
 XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;

complementarity determining region; antibacterial; antiinflammatory.
 Homo sapiens.
 Location/Qualifiers
 43..54
 /label= CDR1
 69..75
 /label= CDR2
 108..116
 /label= CDR3
 EPI222929-A2.
 17-JUL-2002.
 11-JAN-2002; 2002EP-00447005.
 11-JAN-2001; 2001US-0261405P.
 (COLL-) COLLEN RES FOUND VZW D.
 Jacquemin MG, Saint-Remy JR;
 WPI; 2002-610270/66.
 N-PSDB; AAL49255.
 Pharmaceutical composition for treating systemic inflammatory response
 syndrome, sepsis, septic shock and/or thrombus formation in
 microvasculature in mammals, comprises a partial inhibitor of factor
 VIII.
 Disclosure; Fig 11; 41pp; English.
 The present invention relates to a pharmaceutical composition for the
 prevention and/or treatment of systemic inflammatory response syndrome
 (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 and disseminated intravascular coagulation in mammals, comprising as an
 active ingredient a partial inhibitor of factor VIII, in admixture with a
 carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 present sequence is the light chain variable region of B02C11

Query Match 88.7%; Score 654.5; DB 5; Length 142;
 Best Local Similarity 89.5%; Pred. No. 4.4e-41;
 Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITF 120
 DB 61 PGQAPRLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSA-ITF 119
 QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
 DB 120 GQGTREIKGTVAAPSVFIFPPS 142
 RESULT 11
 AA0193704
 ID AA0193704 standard; protein; 233 AA.
 XX AA0193704;
 AC AA0193704;
 XX 03-OCT-2000 (first entry)
 DT The kappa chain of immunoglobulin clone 4.8.1.
 DE
 XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;

KW proliferative disorder; cancer; immunodeficient disorder.
XX Homo sapiens.
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46867.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX Claim 3; Fig 1B; 157pp; English.
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-PR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX SQ Sequence 233 AA;
Query Match 88.7%; Score 654.5; DB 3; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;
QY 1 METPAQLLFLLMLPDTTGEIVLTQPGTLLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLMLPDTTGEIVLTQPGTLLSPGERATLSCRT--SVSSSYLAWYQOK 59
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYVYQYQYGSALTFF 120
Db 59 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYVYQYQYGISP-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 118 GGGTKVEIKRTVAAPSVFIFPPS 140
RESULT 12
AA93731
ID AA93731 standard; protein; 233 AA.
XX AC AA93731;
XX 03-OCT-2000 (first entry)
XX The kappa chain of immunoglobulin clone 4.8.1.
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX Homo sapiens.
OS

XX Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46895.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX Claim 3; Fig 22k; 157pp; English.
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-PR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX SQ Sequence 233 AA;
Query Match 88.7%; Score 654.5; DB 3; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;
QY 1 METPAQLLFLLMLPDTTGEIVLTQPGTLLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLMLPDTTGEIVLTQPGTLLSPGERATLSCRT--SVSSSYLAWYQOK 58
QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYVYQYQYGSALTFF 120
Db 59 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYVYQYQYGISP-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 118 GGGTKVEIKRTVAAPSVFIFPPS 140
RESULT 13
AAE35886
ID AAE35886 standard; protein; 233 AA.
XX AC AAE35886;
XX 17-JUN-2003 (first entry)
XX Human 4.8.1 anti-CTLA-4 antibody kappa chain.
XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
XX cancer.
XX Homo sapiens.
OS

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XX PH Key Location/Qualifiers
XX PT Peptide 1-20
XX FT /label= Signal_peptide
XX FT Protein 21..233
XX XX /note= "Mature anti-CTLA-4 antibody kappa chain"
XX FN EPI262193-A1.
XX PD 04-DEC-2002.
XX PF 23-MAY-2002; 2002EP-00253652.
XX PR 23-MAY-2001; 2001US-0293042P.
XX PA (PRIZ ) PFIZER PROD INC.
XX PI Hanson DC, Mueller EE;
XX DR WPI; 2003-131215/13.
XX DR N-PSDB; AAD54346.
XX PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
XX FT preparation of medicament for the treatment of cancer.
XX PS Disclosure; Fig 1K; 76pp; English.
XX CC The invention relates to the use of human anti-cytotoxic T lymphocyte
XX CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
XX CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
XX CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
XX CC cancer, cancer of the anal region, stomach cancer, breast cancer,
XX CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
XX CC The present sequence is human anti-CTLA-4 antibody kappa chain
XX SQ Sequence 233 AA;

Query Match 88.7%; Score 654.5; DB 6; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

Qy 1 METPAQLLFLLLMLPDTTGEIVLTQPGTILSLSPGERATILSCRASQSVASAYLAWYQOK 60
Dy 1 METPAQLLFLLLMLPDTTGEIVLTQPGTILSLSPGERATILSCRT--SVSSSLAWYQOK 58
Qy 61 PGQAPRLIYGASSRATDIPRFGSGSGTDTLTISRLEPEDFAVYCCQYGTGSLTF 120
Dy 59 PGQAPRLIYGASSRATGIPRFGSGSGTDTLTISRLEPEDFAVYCCQYGTGSLTF 117
Qy 121 GGGTKVEIKRTVAAPSVFIFFPS 143
Dy 118 GGGTKVEIKRTVAAPSVFIFFPS 140

RESULT 14
AAU74301
ID AAU74301 standard; protein; 236 AA.
XX AC AAU74301;
XX DT 12-MAR-2002 (first entry)
XX DE Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
XX KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
XX KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
XX KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
XX KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
XX KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
XX KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
XX KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
XX KW systemic lupus erythematosus; autoimmune disorder; inflammation;
XX KW graft versus host reaction; immune rejection; intestinal immunity;

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KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX OS Homo sapiens.
XX PN WO200187981-A2.
XX PD 22-NOV-2001.
XX PF 15-MAY-2001; 2001WO-JP004035.
XX PR 18-MAY-2000; 2000JP-00147116.
XX PR 30-MAR-2001; 2001JP-00699508.
XX PA (NISB ) JAPAN TOBACCO INC.
XX PI Tsuji T, Tezuka K, Hori N;
XX DR WPI; 2002-075313/10.
XX DR N-PSDB; AAS99477.
XX PT New human monoclonal antibody that binds to activation inducible
XX FT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
XX PT arthritis, multiple sclerosis and inflammation.
XX PS Claim 30; Page 298-299; 300pp; English.
XX CC The invention relates to a novel human antibody (I), preferably a human
XX CC monoclonal antibody which binds to an activation inducible lymphocyte
XX CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
XX CC transduction into a cell mediated by AILIM, for modulating proliferation
XX CC of AILIM-expressing cells, for modulating production of a cytokine from
XX CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
XX CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
XX CC AILIM-expressing cells. (I) is useful for treating, preventing or
XX CC prophylaxis of delayed type allergy. (I) is useful for treating and
XX CC preventing various diseases associated with AILIM-mediated costimulatory
XX CC transduction, and for inhibiting the onset and/or advancement of the
XX CC diseases. (I) is useful for suppression, prevention and/or treatment of
XX CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
XX CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
XX CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
XX CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
XX CC host reaction, graft versus host disease, immune rejection, disorders
XX CC caused by abnormal intestinal immunity, specifically inflammatory
XX CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
XX CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
XX CC immunorejection due to antigenicity to human, i.e., human anti-mouse
XX CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
XX CC AILIM monoclonal antibody amino acid sequences of the invention
XX SQ Sequence 236 AA;

Query Match 88.3%; Score 652; DB 5; Length 236;
Best Local Similarity 88.1%; Pred. No. 1.1e-40;
Matches 126; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METPAQLLFLLLMLPDTTGEIVLTQPGTILSLSPGERATILSCRASQSVASAYLAWYQOK 60
Dy 1 METPAQLLFLLLMLPDTTGEIVLTQPGTILSLSPGERATILSCRASQSVSSSLAWYQOK 60
Qy 61 PGQAPRLIYGASSRATDIPRFGSGSGTDTLTISRLEPEDFAVYCCQYGTGSLTF 120
Dy 61 PGQAPRLIYGASSRATGIPRFGSGSGTDTLTISRLEPEDFAVYCCQYGTGSLTF 120
Qy 121 GGGTKVEIKRTVAAPSVFIFFPS 143
Dy 121 GGGTKLEIKRTVAAPSVFIFFPS 143

RESULT 15
AAW40069
ID AAW40069 standard; protein; 150 AA.
XX XX

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Search completed: April 5, 2004, 13:24:17
Job time : 46.2149 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 33.6328 Seconds
(without alignments)
1116.513 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738
Sequence: 1 METPAQLFLLLWLPDTTG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	738	100.0	143	14	US-10-044-569B-8
2	666.5	90.3	235	14	US-10-153-382-7
3	660	89.4	236	9	US-09-859-053-34
4	659.5	89.2	235	12	US-10-180-548-4
5	654.5	88.7	142	14	US-10-044-569B-4
6	654.5	88.7	233	14	US-10-153-382-11
7	652	88.3	236	9	US-09-859-053-38
8	649.5	88.0	150	10	US-09-782-397-5
9	645	87.4	234	14	US-10-153-382-15
10	609	82.5	236	11	US-09-833-245-237
11	596	80.8	127	15	US-10-309-762-95
12	593.5	80.4	128	15	US-10-309-764-89
13	593	80.4	127	15	US-10-309-762-91
14	592	80.2	127	15	US-10-309-762-93
15	585	79.3	234	10	US-09-848-832-4
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					Sequence 7, Appli
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					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 11, Appli
					Sequence 38, Appli
					Sequence 5, Appli
					Sequence 15, Appli
					Sequence 237, Appli
					Sequence 95, Appli
					Sequence 89, Appli
					Sequence 91, Appli
					Sequence 93, Appli
					Sequence 4, Appli

16	585	79.3	234	14	US-10-225-108A-4
17	585	79.3	234	15	US-10-461-148-2
18	575.5	78.0	384	15	US-10-291-265-804
19	575.5	78.0	384	15	US-10-291-265-805
20	575.5	78.0	384	15	US-10-291-265-806
21	575.5	78.0	384	15	US-10-291-265-807
22	575	77.9	226	10	US-09-453-234-42
23	571	77.4	226	10	US-09-453-234-50
24	569	77.1	226	10	US-09-453-234-86
25	569	77.1	226	10	US-09-453-234-80
26	566	76.8	224	10	US-09-453-234-52
27	566	76.7	226	10	US-09-453-234-72
28	565.5	76.6	215	15	US-10-307-724-122
29	564	76.4	226	10	US-09-453-234-38
30	559.5	75.8	307	15	US-10-291-265-332
31	559.5	75.8	312	15	US-09-453-234-34
32	559	75.7	226	10	US-09-453-234-74
33	558	75.6	129	15	US-10-309-764-121
34	556	75.3	129	15	US-10-309-764-105
35	554	75.1	224	10	US-09-453-234-76
36	553.5	75.0	215	10	US-09-791-153A-49
37	553	74.9	129	15	US-10-309-764-141
38	553	74.9	224	10	US-09-453-234-44
39	553	74.9	224	10	US-09-453-234-78
40	552	74.8	238	14	US-10-216-484-107
41	552	74.8	238	14	US-10-384-933-107
42	549	74.4	129	15	US-10-309-764-97
43	549	74.4	224	10	US-09-453-234-40
44	545.5	73.9	130	15	US-10-443-466A-25
45	543	73.6	129	15	US-10-309-764-101

ALIGNMENTS

RESULT 1
US-10-044-569B-8
; Sequence 8, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PST
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (127)..(162)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (205)..(225)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (325)..(354)
; OTHER INFORMATION: complementary determining region number three
US-10-044-569B-8

Query Match 100.0%; Score 738; DB 14; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match      89.4%; Score 660; DB 9; Length 236;
Best Local Similarity 88.8%; Pred. No. 1.7e-49;
Matches 127; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60

QY 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
Db 121 GGGTKVEIKRTVAAPSVFIPIPPS 143

RESULT 2
US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-7

Query Match      90.3%; Score 666.5; DB 14; Length 235;
Best Local Similarity 91.6%; Pred. No. 4.6e-50;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60

QY 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
Db 120 GGGTKVEIKRTVAAPSVFIPIPPS 142

RESULT 3
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

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Best Local Similarity 88.8%; Pred. No. 1.7e-49;
Matches 127; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60

QY 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
Db 121 GGGTKVEIKRTVAAPSVFIPIPPS 143

RESULT 4
US-10-180-648-4
; Sequence 4, Application US/10180648
; Publication No. US2004003353A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvatan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-4

Query Match      89.2%; Score 658.5; DB 12; Length 235;
Best Local Similarity 91.6%; Pred. No. 2.2e-49;
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QY 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPTTGTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60

QY 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQAPRLLIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
Db 120 GGGTKVEIKRTVAAPSVFIPIPPS 142

RESULT 5
US-10-044-569B-4
; Sequence 4, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
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;; CURRENT FILING DATE: 2002-01-11
;; PRIOR APPLICATION NUMBER: US 60/261,405
;; PRIOR FILING DATE: 2001-01-11
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 4
;; LENGTH: 142
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (127)..(162)
;; OTHER INFORMATION: complementary determining region number one
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;; NAME/KEY: misc feature
;; LOCATION: (205)..(225)
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;; LOCATION: (325)..(351)
;; OTHER INFORMATION: complementary determining region number three
US-10-044-569b-4

Query Match 88.7%; Score 654.5; DB 14; Length 142;
Best Local Similarity 89.5%; Pred. No. 2.9e-49;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
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DB 61 PQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSA-ITF 119
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 120 GQGRLEIKGTVAAPSVFIIPPS 142

RESULT 6
US-10-153-382-11
;; Sequence 11, Application US/10153382
;; Publication No. US20030086930A1
;; GENERAL INFORMATION:
;; APPLICANT: PFIZER PRODUCTS INC.
;; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;; FILE REFERENCE: PC23019A
;; CURRENT APPLICATION NUMBER: US/10/153,382
;; CURRENT FILING DATE: 2002-05-22
;; PRIOR APPLICATION NUMBER: 60/293042
;; PRIOR FILING DATE: 2001-05-23
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 11
;; LENGTH: 233
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-153-382-11

Query Match 88.7%; Score 654.5; DB 14; Length 233;
Best Local Similarity 91.6%; Pred. No. 4.9e-49;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;
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DB 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSCT--SVSSVYAWYQOK 58
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
DB 59 PQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSP-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143

DB 118 GGGTKVEIKRTVAAPSVFIIPPS 140

RESULT 7
US-09-859-053-38
;; Sequence 38, Application US/09859053
;; Patent No. US20020102658A1
;; GENERAL INFORMATION:
;; APPLICANT: Tezuka, Takashi
;; APPLICANT: Tezuka, Katsumari
;; APPLICANT: Hori, No. US20020102658A1uaki
;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;; OTHER INFORMATION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
;; FILE REFERENCE: 06501-079001
;; CURRENT APPLICATION NUMBER: US/09/859,053
;; CURRENT FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: JP 2001-99508
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: JP 2000-147116
;; PRIOR FILING DATE: 2000-05-18
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 38
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-859-053-38

Query Match 88.3%; Score 652; DB 9; Length 236;
Best Local Similarity 88.1%; Pred. No. 8.3e-49;
Matches 126; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
DB 61 PQAPGLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 121 GQGRLEIKGTVAAPSVFIIPPS 143

RESULT 8
US-09-782-397-5
;; Sequence 5, Application US/09782397
;; Publication No. US20030021779A1
;; GENERAL INFORMATION:
;; APPLICANT: Dan, Michael D.
;; Maity, Pradip K.
;; Kaplan, Howard A.
;; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
;; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;; DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Morisson & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```
;; APPLICATION NUMBER: US/09/782,397
;; FILING DATE: 13-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/862,124
;; FILING DATE: 1997-05-22
;; ATTORNEY/AGENT INFORMATION:
;; NAME, Lehabardt, Susan K.
;; REGISTRATION NUMBER: 33,943
;; REFERENCE/DOCKET NUMBER: 31608-20001.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 813-5600
;; TELEFAX: (650) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 150 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-782-397-5
Query Match      88.0%; Score 649.5; DB 10; Length 150;
Best Local Similarity 87.7%; Pred. No. 8.4e-49;
Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 METPAQLLEFLLLLPDPTTGTEIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 5 MEFOQALLFLLLLPDITGDIVLTQSPGTILSPGERATILSCRASQSVSSYLAWYQOK 64

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFPAVYCCQYGTSS---AL 117
DB 65 PQQAPRLIYGASTRATGMPDRFSGSGGTDFTLTISRLEPEDFPAVYCCQYGTSSPQTPQ 124

QY 118 LTFGGGTVKVKRTVAAPSVFIFFPS 143
DB 125 ITFGGTVKVKRTVAAPSVFIFFPS 150

RESULT 9
US-10-153-382-15
; Sequence 15, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-15
Query Match      87.4%; Score 645; DB 14; Length 234;
Best Local Similarity 90.9%; Pred. No. 3.3e-48;
Matches 130; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

QY 1 METPAQLLEFLLLLPDPTTGTEIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLLEFLLLLPDPTTGTEIVLTQSPGTILSPGERATILSCRASQSV-SSYLAWYQOK 59

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFPAVYCCQYGTSSALLTF 120
DB 60 PQQAPRLIYGSSRATGIPDRFSGSGGTDFTLTISRLEPEDFPAVYCCQYGTSS-FTF 118

QY 121 GGGTKVEIKRTVAAPSVFIFFPS 143
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DB 119 GPGTKVDIKRTVAAPSVFIFFPS 141

RESULT 10
US-09-833-245-237
; Sequence 237, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 237
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237
Query Match      82.5%; Score 609; DB 11; Length 236;
Best Local Similarity 86.8%; Pred. No. 4.4e-45;
Matches 125; Conservative 1; Mismatches 16; Indels 2; Gaps 2;
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QY 1 METPAQLLEFLLLLPDPTTGTEIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 1 MEXPAQLLEFLLLLPDPTTGTEIVLTQSPXTILSPGERATILSCRASQSV-SSYLAWYQOK 59

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFPAVYCCQYGTSSALLT 119
DB 60 PQQAPRLIYGASXRATGIPXRFSGSGGTDFTLTISRLEPEDFPAVYCCQXNPPXYT 119

QY 120 FGGTKVEIKRTVAAPSVFIFFPS 143
DB 120 FGXGTVKVKRTVAAPSVFIFFPS 143
```

```
RESULT 11
US-10-309-762-95
; Sequence 95, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-95

Query Match      80.4%; Score 596; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 3.1e-44;
Matches 118; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 MEAPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 120
Db 61 PGQAPRLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 118

QY 121 GGGTKVEIK 129
Db 119 GGGTKVEIK 127

RESULT 12
US-10-309-764-89
; Sequence 89, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: AGENIX 029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-764-89

Query Match      80.4%; Score 593.5; DB 15; Length 128;
Best Local Similarity 91.5%; Pred. No. 5.1e-44;
Matches 118; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSISSALAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 120
Db 61 PGQAPRLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 118

QY 121 GGGTKVEIK 129
Db 119 GGGTKVEIK 127

RESULT 13
US-10-309-762-91
; Sequence 91, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-91

Query Match      80.4%; Score 593; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 5.6e-44;
Matches 118; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 MEAPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 120
Db 61 PGQAPRLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 118

QY 121 GGGTKVEIK 129
Db 119 GGGTKVEIK 127

RESULT 14
US-10-309-762-93
; Sequence 93, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-93
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```
US-10-309-762-93
Query Match      80.2%; Score 592; DB 15; Length 127;
Best Local Similarity 90.7%; Pred. No. 6.8e-44;
Matches 117; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPLDPTTGEIVLTQFPGLTSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
Db 1 METPAQLLFLLLWLPLDPTTGEIVLTQSPGLTSLSPGERATLSCRSTQTVYSTYLAWYQOK 60
   |||||

QY 61 PQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYCTSAALLTF 120
   |||||
Db 61 PQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYCTSAALLTF 118
   |||||

QY 121 GGTGKVEIK 129
   |||||
Db 119 GGTGKVEIK 127
   |||||

RESULT 15
US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-4

Query Match      79.3%; Score 585; DB 10; Length 234;
Best Local Similarity 83.9%; Pred. No. 5.3e-43;
Matches 120; Conservative 5; Mismatches 16; Indels 2; Gaps 2;

QY 1 METPAQLLFLLLWLPLDPTTGEIVLTQFPGLTSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
Db 1 MEAPQALLFLLLWLPLDPTTGEIVLTQSPATLSPGERATLACRASQT-ASRYLAWYQOK 59
   |||||

QY 61 PQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYCTSAALLTF 120
   |||||
Db 60 PQAPRLLIYDTSNRATGIPARFSGSGGTDFTLTISRLEPEDFAVYCCQ-RFNWPWTF 118
   |||||

QY 121 GGTGKVEIKRTVAAPSVFIFPPS 143
   |||||
Db 119 GGTGKVEIKRTVAAPSVFIFPPS 141
   |||||

Search completed: April 5, 2004, 13:59:14
Job time : 33.6328 secs
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